

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 16.403 Seconds  
(without alignments)  
120.578 Million cell updates/sec

Title: US-09-641-802-1  
Perfect score: 42  
Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	42	100.0	7	4	AAB72500	Aab72500 Colostrin
2	42	100.0	7	4	AAB59324	Aab59324 Ewe colos
3	42	100.0	7	4	AAB72246	Aab72246 Colostrin
4	42	100.0	7	4	AAB72532	Aab72532 Colostrin
5	42	100.0	7	5	AAO14577	Aao14577 Neural ce
6	42	100.0	7	5	AAM51036	Aam51036 Colostrin
7	42	100.0	7	5	AAE20228	Aae20228 Colostrin
8	42	100.0	8	4	AAB59354	Aab59354 Ewe colos
9	36	85.7	12	7	ADC36090	Adc36090 Chemokine

10	34	81.0	12	6	AAE32821	Aae32821	Human CEA
11	34	81.0	15	3	AAy85491	Aay85491	Human ced
12	34	81.0	16	3	AAy85494	Aay85494	Human ced
13	33	78.6	7	4	AAM46973	Aam46973	H11 bindi
14	33	78.6	10	2	AAW06853	Aaw06853	Peptide b
15	33	78.6	11	3	AAB21127	Aab21127	Src homol
16	33	78.6	12	2	AAW06845	Aaw06845	Peptide b
17	33	78.6	13	2	AAW38072	Aaw38072	PPPPY mot
18	33	78.6	13	7	ADB49333	Adb49333	Biotinyln
19	32	76.2	7	2	AAR60997	Aar60997	Fragment
20	32	76.2	7	2	AAR91752	Aar91752	Prolyl en
21	32	76.2	7	4	AAM46827	Aam46827	H11 bindi
22	32	76.2	7	4	AAM46861	Aam46861	H11 bindi
23	32	76.2	7	4	AAM46876	Aam46876	H11 bindi
24	32	76.2	7	4	AAM47027	Aam47027	H11 bindi
25	32	76.2	7	4	AAM46856	Aam46856	H11 bindi
26	32	76.2	7	4	AAM46871	Aam46871	H11 bindi
27	32	76.2	7	4	AAM46851	Aam46851	H11 bindi
28	32	76.2	7	4	AAM46866	Aam46866	H11 bindi
29	32	76.2	8	2	AAR71945	Aar71945	Human 3BP
30	32	76.2	10	2	AAR77371	Aar77371	SH3 bindi
31	32	76.2	10	2	AAW06861	Aaw06861	Peptide b
32	32	76.2	10	2	AAW38097	Aaw38097	PPPPY mot
33	32	76.2	10	2	AAW38074	Aaw38074	PPPPY mot
34	32	76.2	10	4	AAB86131	Aab86131	Proline-r
35	32	76.2	10	4	AAB86149	Aab86149	Proline-r
36	32	76.2	10	4	AAB70933	Aab70933	Polyoma v
37	32	76.2	10	7	ADB49372	Adb49372	Biotinyln
38	32	76.2	10	7	ADB49335	Adb49335	Biotinyln
39	32	76.2	11	3	AAB21129	Aab21129	Src homol
40	32	76.2	11	3	AAB21132	Aab21132	Src homol
41	32	76.2	11	3	AAB21126	Aab21126	Src homol
42	32	76.2	11	5	ABB99165	Abb99165	Formin-2
43	32	76.2	11	5	ABB99166	Abb99166	Formin-2
44	32	76.2	12	2	AAW03154	Aaw03154	Potential
45	32	76.2	12	2	AAW05101	Aaw05101	Proline-r
46	32	76.2	12	2	AAW25457	Aaw25457	SH3 domai
47	32	76.2	12	3	AAB18002	Aab18002	Fc-TNF al
48	32	76.2	12	6	ADA50131	Ada50131	Mad2 bind
49	32	76.2	13	2	AAR84641	Aar84641	Grb2-SOS
50	32	76.2	13	4	AAB70928	Aab70928	Polyoma v
51	32	76.2	13	6	ABU10225	Abu10225	Human cyt
52	32	76.2	13	7	AAE39883	Aae39883	Human cyt
53	32	76.2	14	2	AAW05490	Aaw05490	SH3-bindi
54	32	76.2	14	2	AAW38067	Aaw38067	PPPPY mot
55	32	76.2	14	7	ADB49257	Adb49257	Biotinyln
56	32	76.2	15	2	AAW39034	Aaw39034	Peptide r
57	32	76.2	15	2	AAW39005	Aaw39005	Peptide r
58	32	76.2	15	2	AAW39050	Aaw39050	Peptide r
59	32	76.2	15	2	AAW38988	Aaw38988	Peptide r
60	32	76.2	15	2	AAW39035	Aaw39035	Peptide r
61	32	76.2	15	2	AAW38959	Aaw38959	Peptide r
62	32	76.2	15	2	AAW39015	Aaw39015	Peptide r
63	32	76.2	15	2	AAW39040	Aaw39040	Peptide r
64	32	76.2	15	2	AAy41635	Aay41635	Mammalian
65	32	76.2	16	2	AAW25411	Aaw25411	Crk N-ter
66	32	76.2	17	2	AAW38977	Aaw38977	Peptide r

67	32	76.2	17	2	AAW38963	Aaw38963	Peptide r
68	32	76.2	18	2	AAR91750	Aar91750	Prolyl en
69	32	76.2	18	2	AAR91746	Aar91746	Prolyl en
70	32	76.2	18	2	AAW38923	Aaw38923	Peptide r
71	32	76.2	18	2	AAW39010	Aaw39010	Peptide r
72	31	73.8	12	3	AAY56628	Aay56628	Virus-lik
73	31	73.8	12	3	AAY56271	Aay56271	Human cat
74	31	73.8	13	2	AAW05447	Aaw05447	SH3-bindi
75	31	73.8	13	2	AAW37655	Aaw37655	PPPPY mot
76	31	73.8	13	7	ADB49202	Adb49202	Biotinyla
77	31	73.8	13	7	ADB49281	Adb49281	Novel WW
78	31	73.8	14	3	ADC16813	Adc16813	Human sin
79	31	73.8	15	2	AAW38905	Aaw38905	Peptide r
80	31	73.8	16	2	AAW38947	Aaw38947	Peptide r
81	31	73.8	17	2	AAW38104	Aaw38104	Peptide r
82	31	73.8	17	7	ADB49204	Adb49204	Biotinyla
83	30	71.4	7	4	AAM47005	Aam47005	H11 bindi
84	30	71.4	7	4	AAM47010	Aam47010	H11 bindi
85	30	71.4	9	2	AAR60998	Aar60998	Sequence
86	30	71.4	9	6	ABR28254	Abr28254	Human can
87	30	71.4	9	6	ABR28252	Abr28252	Human can
88	30	71.4	9	6	ABR27236	Abr27236	Human can
89	30	71.4	10	2	AAR93318	Aar93318	ABL prote
90	30	71.4	10	2	AAR93322	Aar93322	ABL prote
91	30	71.4	10	2	AAR93342	Aar93342	TSK prote
92	30	71.4	10	2	AAR93319	Aar93319	ABL prote
93	30	71.4	10	2	AAR93320	Aar93320	ABL prote
94	30	71.4	10	2	AAR93339	Aar93339	TSK prote
95	30	71.4	10	2	AAR93321	Aar93321	ABL prote
96	30	71.4	10	2	AAR93340	Aar93340	TSK prote
97	30	71.4	10	2	AAR93317	Aar93317	ABL prote
98	30	71.4	10	2	AAR93314	Aar93314	ABL prote
99	30	71.4	10	2	AAR93315	Aar93315	ABL prote
100	30	71.4	10	2	AAR93316	Aar93316	ABL prote

# ALIGNMENTS

## RESULT 1

AAB72500

ID AAB72500 standard; peptide; 7 AA.

XX

AC AAB72500;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #1.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.  
 XX  
 PR 17-AUG-1999; 99US-0149310P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the cell  
 PT with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations.  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 |||||  
 Db 1 MQPPPLP 7

## RESULT 2

AAB59324

ID AAB59324 standard; peptide; 7 AA.

XX

AC AAB59324;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment B-9.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.



XX  
PA (REGE-) REGEN THERAPEUTICS PLC.  
XX  
PI Georgiades JA;  
XX  
DR WPI; 2001-071058/08.  
XX  
PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.  
XX  
PS Claim 7; Page 27; 63pp; English.  
XX  
CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
| | | | |  
Db 1 MQPPPLP 7

RESULT 3  
AAB72246

ID AAB72246 standard; peptide; 7 AA.  
XX  
AC AAB72246;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 1.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
PN WO200111937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US022818.  
XX

PR 17-AUG-1999; 99US-0149311P.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX

DR WPI; 2001-202804/20.

XX

PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator.

XX

PS Claim 1; Page 34; 50pp; English.

XX

CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The peptides  
CC have immune response modulatory activity, and are capable of inducing  
CC cytokines. Colostrinin and its derived peptides are useful for inducing  
CC cytokine production, for modulating an immunological response and for  
CC inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7

||||||

Db 1 MQPPPLP 7

#### RESULT 4

AAB72532

ID AAB72532 standard; peptide; 7 AA.

XX

AC AAB72532;

XX

DT 09-MAY-2001. (first entry)

XX

DE Colostrinin peptide #1.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX

PD 22-FEB-2001.

XX  
 PF 17-AUG-2000; 2000WO-US022774.  
 XX  
 PR 17-AUG-1999; 99US-0149633P.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating damaged  
 PT neural cells in a patient.  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 |||||  
 Db 1 MQPPPLP 7

RESULT 5

AA014577

ID AA014577 standard; peptide; 7 AA.

XX

AC AA014577;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 1.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 7

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
CC polypeptide aggregate that is present in colostrum. The method of the  
CC invention is useful for promoting the differentiation of cells and for  
CC treating damaged neural cells in a patient. The present amino acid  
CC sequence represents a specifically claimed colostrinin peptide used in  
CC the method of the invention

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

|||||||

Db 1 MQPPPLP 7

#### RESULT 6

AAM51036

ID AAM51036 standard; peptide; 7 AA.

XX

AC AAM51036;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; beta-casein; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 7

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US022775.  
 XX  
 PR 17-AUG-2000; 2000WO-US022775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2002-269150/31.  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of blood  
 PT cell regulator selected from colostrinin, its constituent peptide and/or  
 PT analog.  
 XX  
 PS Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide that is  
 CC preferred for use as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified as having  
 CC a beta-casein homologue precursor. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator, where the  
 CC cell is present in a cell culture, a tissue, an organ or an organism, and  
 CC the cell is mammalian, including human; modulating an immune response in  
 CC a cell by contact with the immunological regulator under conditions  
 CC effective to induce a cytokine; modulating an immune response in a  
 CC patient by administering an immunological regulator under conditions  
 CC effective to induce a cytokine, where the immunological regulator is  
 CC administered topically or as part of a dietary supplement, and where the  
 CC immune response is specific or non specific, an interferon response or an  
 CC antibody response; modulating blood cell proliferation by contacting  
 CC blood cells with a blood cell regulator, where the blood cells are  
 CC present in a cell culture or an organism, are mammalian or human, and  
 CC where the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A claimed  
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an  
 CC active agent such as the present peptide. Cytokines induced by this  
 CC peptide in human leucocyte cultures include interferon-gamma, tumour  
 CC necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and  
 CC interleukin-12. It was one of the best overall inducers in almost all  
 CC cytokine and blood cell proliferation experiments conducted  
 XX  
 SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
 |||||  
 Db 1 MQPPPLP 7

RESULT 7

AAE20228

ID AAE20228 standard; peptide; 7 AA.

XX

AC AAE20228;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #1.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 7

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 25; 51pp; English.

XX

CC The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress level  
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,  
CC organ, or organism; or for treating oxidative damage to the skin of a  
CC patient e.g. animal or human; to modulate oxidative stress during/ after  
CC a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidising species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present

CC sequence is a colostrinin constituent peptide

XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 42; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

|||||||

Db 1 MQPPPLP 7

#### RESULT 8

AAB59354

ID AAB59354 standard; peptide; 8 AA.

XX

AC AAB59354;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #14.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system and  
PT immune system, viral and bacterial infections, and diseases characterized  
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 42; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7

||||||

Db 2 MQPPPLP 8

#### RESULT 9

ADC36090

ID ADC36090 standard; peptide; 12 AA.

XX

AC ADC36090;

XX

DT 18-DEC-2003 (first entry)

XX

DE Chemokine binding peptide BKT-P4.

XX

KW peptidic chemokine modulator; antiinflammatory; antiallergic;  
KW immunosuppressive; antidiabetic; antirheumatic; dermatological;  
KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;  
KW antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotropic;  
KW cytostatic; inflammation; allergy; immune response; autoimmune reaction;  
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;  
KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;  
KW hypertension; reperfusion ischaemia.

XX

OS Synthetic.

XX

PN WO2003072599-A2.

XX

PD 04-SEP-2003.

XX

PF 27-FEB-2003; 2003WO-IL000155.

XX

PR 28-FEB-2002; 2002US-0359995P.

XX

PA (BIOK-) BIOKINE THERAPEUTICS LTD.

XX

PI Peled A, Eizenberg O, Vaizel-Ohayon D;

XX

DR WPI; 2003-671869/63.

XX

PT New peptidic chemokine modulator, useful for preparing a composition for  
PT treating a disease modulated through and/or caused by binding of a  
PT chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis  
PT or cancer.

XX

PS Example 1; Page 28; 43pp; English.

XX

CC The present invention describes a peptidic chemokine modulator (I) for  
CC modulating a biological effect of a chemokine. (I) comprises a molecule



CC consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr  
 CC and Pro, and features at least 2 histidines spread along the molecule,  
 CC where the molecule features an overall positive charge (family 1); or (b)  
 CC the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two  
 CC neighbouring histidines, where the molecule features an overall positive  
 CC charge (family 2). Also described: (1) 'a composition for treating a  
 CC condition involving abnormal cell migration in a subject; (2) a method  
 CC for treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor in a subject; (3) an antibody for  
 CC binding to a chemokine-binding receptor that recognises at least a  
 CC portion of a chemokine-binding receptor or the peptide; (4) a vaccine  
 CC formed with the antibody; and (5) a method for producing an antibody. (I)  
 CC has antiinflammatory, antiallergic, immunosuppressive, antidiabetic,  
 CC antirheumatic, dermatological, antiarthritic, antibacterial,  
 CC antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive,  
 CC neuroprotective, virucide, vasotropic and cytostatic activities. The  
 CC peptidic chemokine modulator is useful for preparing a composition for  
 CC treating a disease modulated through and/or caused by binding of a  
 CC chemokine to a chemokine receptor, comprising inflammation (primary or  
 CC secondary), allergy, a non-optimal immune response, an autoimmune  
 CC reaction (including rheumatoid arthritis, systemic lupus erythematosus,  
 CC multiple sclerosis and others), allograft rejection, diabetes, sepsis,  
 CC cancer and any type of malignant cell growth, acne and chronic bacterial  
 CC and viral infections, arthritis, colitis, psoriasis, atherosclerosis,  
 CC hypertension or reperfusion ischaemia. The present sequence represents a  
 CC chemokine binding peptide, which is used in an example from the present  
 CC invention.

XX

SQ Sequence 12 AA;

Query Match 85.7%; Score 36; DB 7; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
 | | | | |  
 Db 5 MQPPPRP 11

# RESULT 10

AAE32821

ID AAE32821 standard; peptide; 12 AA.

XX

AC AAE32821;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human CEA exon #24 encoded peptide.

XX

KW Human; carcinoembryonic antigen; CEA; cell adhesion-mediated disease;  
 KW prognosis; cancer; tumour; gene therapy; exon.

XX

OS Homo sapiens.

XX

PN WO200290508-A2.

XX

PD 14-NOV-2002.

XX  
 PF 07-MAY-2002; 2002WO-US014457.  
 XX  
 PR 07-MAY-2001; 2001US-0289179P.  
 PR 29-AUG-2001; 2001US-0315736P.  
 XX  
 PA (ALPH-) ALPHAGENE INC.  
 XX  
 PI Stark KA, Weaver A, Hoffmann HM, Krauss R, Valenzuela DB;  
 PI Saini KS;  
 XX  
 DR WPI; 2003-111965/10.  
 XX  
 PT New carcinoembryonic antigen and polynucleotides encoding them, useful  
 PT for treating and/or preventing cell adhesion-mediated disease (e.g.  
 PT cancers, solid tumors, tumor metastasis or benign tumors) symptoms.  
 XX  
 PS Claim 17; Page 130; 143pp; English.  
 XX  
 CC The invention relates to novel human carcinoembryonic antigen (CEA)  
 CC polypeptides and polynucleotides encoding such polypeptides. CEA genes  
 CC are useful as diagnostic and prognostic markers of colon, stomach and  
 CC breast cancers. Polypeptides of the invention can be used to diagnose,  
 CC treat and/or prevent cell adhesion-mediated disease (e.g. cancers, solid  
 CC tumours, tumour metastasis or benign tumours) and to modulate cell-cell  
 CC or cell-matrix adhesion in mammalian tissues. The invention is useful in  
 CC gene therapy. The present sequence is human CEA exon encoded peptide.  
 CC Note: This sequence is stated to be encoded by SEQ ID NO: 52 (AAD50572).  
 CC However this does not appear to be the case  
 XX  
 SQ Sequence 12 AA;  
  
 Query Match 81.0%; Score 34; DB 6; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 1 MQPPPLP 7  
 |||| ||  
 Db 1 MQPPDLP 7  
  
 RESULT 11  
 AAY85491  
 ID AAY85491 standard; peptide; 15 AA.  
 XX  
 AC AAY85491;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE Human ced-6 (hced-6) peptide epitope.  
 XX  
 KW ced-6; hlced-6; h2ced-6; signal transduction pathway; phagocytosis;  
 KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;  
 KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;  
 KW cardiant; immunosuppressive; apoptosis modulator; epitope.  
 XX  
 OS Homo sapiens.

XX  
 PN WO9964586-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004043.  
 XX  
 PR 11-JUN-1998; 98GB-00012660.  
 PR 24-SEP-1998; 98GB-00020816.  
 XX  
 PA (DEVG-) DEVGEN NV.  
 XX  
 PI Smits E, Van Criekinge WMR, Bogaert TAOE;  
 XX  
 DR WPI; 2000-246285/21.  
 XX  
 PT Assays for determining the phagocytosis of apoptotic cells useful for  
 PT identifying a compound which influences the phagocytic uptake of  
 PT apoptotic cells and treats cancers and neurodegenerative diseases.  
 XX  
 PS Claim 62; Page 56; 122pp; English.  
 XX  
 CC The invention relates to assays involving two human homologues of  
 CC Caenorhabditis elegans ced-6 (hlced-6 and h2ced-6) for identifying  
 CC compounds which function as an inhibitor or an enhancer of a signal  
 CC transduction pathway. The assays are carried out by measuring  
 CC phagocytosis of apoptotic cells. The methods are useful for identifying  
 CC compounds which can act as apoptotic modulators which are useful for  
 CC treating diseases such as cancer, autoimmune diseases, neurodegenerative  
 CC diseases such as Huntington's disease, stroke, myocardial infarction and  
 CC AIDS. The assays are well adapted for medium and high throughput  
 CC screening using a multi-well plate format. Sequences AAY85489-91  
 CC represent peptide epitopes of hced-6, used for generating antibodies  
 XX  
 SQ Sequence 15 AA;

Query Match 81.0%; Score 34; DB 3; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 ||||:|  
 Db 6 QPPPVP 11

# RESULT 12

AAY85494

ID AAY85494 standard; peptide; 16 AA.

XX

AC AAY85494;

XX

DT 03-JUL-2000 (first entry)

XX

DE Human ced-6 (hced-6) peptide epitope.

XX

KW ced-6; hlced-6; h2ced-6; signal transduction pathway; phagocytosis;  
 KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;

KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;  
 KW cardiant; immunosuppressive; apoptosis modulator; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9964586-A2.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 10-JUN-1999; 99WO-EP004043.  
 XX  
 PR 11-JUN-1998; 98GB-00012660.  
 PR 24-SEP-1998; 98GB-00020816.  
 XX  
 PA (DEVG-) DEVGEN NV.  
 XX  
 PI Smits E, Van Crieckinge WMR, Bogaert TAOE;  
 XX  
 DR WPI; 2000-246285/21.  
 XX  
 PT Assays for determining the phagocytosis of apoptotic cells useful for  
 PT identifying a compound which influences the phagocytic uptake of  
 PT apoptotic cells and treats cancers and neurodegenerative diseases.  
 XX  
 PS Example 6; Page 35; 122pp; English.  
 XX  
 CC The invention relates to assays involving two human homologues of  
 CC Caenorhabditis elegans ced-6 (hlced-6 and h2ced-6) for identifying  
 CC compounds which function as an inhibitor or an enhancer of a signal  
 CC transduction pathway. The assays are carried out by measuring  
 CC phagocytosis of apoptotic cells. The methods are useful for identifying  
 CC compounds which can act as apoptotic modulators which are useful for  
 CC treating diseases such as cancer, autoimmune diseases, neurodegenerative  
 CC diseases such as Huntington's disease, stroke, myocardial infarction and  
 CC AIDS. The assays are well adapted for medium and high throughput  
 CC screening using a multi-well plate format. Sequences AAY85492-94  
 CC represent peptide epitopes of hced-6, used for generating polyclonal  
 CC antibodies  
 XX  
 SQ Sequence 16 AA;

Query Match 81.0%; Score 34; DB 3; Length 16;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 ||||:|  
 Db 7 QPPVP 12

RESULT 13  
 AAM46973  
 ID AAM46973 standard; peptide; 7 AA.  
 XX  
 AC AAM46973;  
 XX  
 DT 25-OCT-2001 (first entry)

XX  
 DE H11 binding site consensus conforming peptide (CCP) #3244.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-02290722.  
 XX  
 PR 08-DEC-1999; 99CA-02290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX  
 PS Example 4; Page 112; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 78.6%; Score 33; DB 4; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7

Db                   :|||||  
                      2 RPPPLP 7

RESULT 14

AAW06853

ID    AAW06853 standard; peptide; 10 AA.

XX

AC    AAW06853;

XX

DT    16-FEB-1997   (first entry)

XX

DE    Peptide binding the Crk-SH3 domain, used to treat cancer.

XX

KW    Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;

KW    diagnosis; antibody; signal transduction; disease; disorder;

KW    intracellular signalling protein.

XX

OS    Synthetic.

XX

PN    WO9621011-A2.

XX

PD    11-JUL-1996.

XX

PF    28-DEC-1995;    95WO-US016979.

XX

PR    30-DEC-1994;    94US-00367070.

XX

PA    (UYRQ ) UNIV ROCKEFELLER.

XX

PI    Hanafusa H,   Knudsen BS,   Feller SM,   Kuriyan J,   Wu X,   Zheng J;

PI    Cowburn D;

XX

DR    WPI; 1996-333986/33.

XX

PT    New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for

PT    the diagnosis and treatment of defects in intracellular signal

PT    transduction, partic. in cancer.

XX

PS    Claim 3; Page 92; 120pp; English.

XX

CC    New peptides or proteins which comprise these peptides, bind to the Crk-

CC    SH3 domain and competitively inhibit the binding of intracellular

CC    signalling proteins. They can be used in the treatment of a disease or

CC    disorder associated with a defect in intracellular signal transduction,

CC    particularly cancer. They can also be used to diagnose such diseases and

CC    disorders. Antibodies raised against these proteins can be used for the

CC    same purposes. The peptides are derived from the Crk-SH3 binding domains

CC    of intracellular signalling proteins. Peptides related to the invention

CC    are described in AAW03149-63 and AAW06842-W06866

XX

SQ    Sequence 10 AA;

Query Match                   78.6%;   Score 33;   DB 2;   Length 10;

Best Local Similarity   83.3%;   Pred. No. 2.1e+02;

Matches    5;   Conservative    1;   Mismatches    0;   Indels       0;   Gaps       0;

Qy            2 QPPPLP 7  
              :|||||  
Db            1 KPPPLP 6

RESULT 15

AAB21127

ID    AAB21127 standard; peptide; 11 AA.

XX

AC    AAB21127;

XX

DT    19-JAN-2001    (first entry)

XX

DE    Src homology 3 domain binding peptide #4.

XX

KW    Src homology domain 3; SH3; protein-protein interaction; cancer;

KW    signal transduction inhibition; immune suppression-associated disease.

XX

OS    Synthetic.

XX

PN    WO200047607-A1.

XX

PD    17-AUG-2000.

XX

PF    12-FEB-2000; 2000WO-KR000107.

XX

PR    12-FEB-1999;    99AU-00008643.

PR    02-JUN-1999;    99KR-00020282.

XX

PA    (YOON/) YOON J H.

PA    (HANY/) HAN Y T.

XX

PI    Yoon JH,    Han YT,    Lee KY;

XX

DR    WPI; 2000-533010/48.

XX

PT    Synthetic peptides useful for treating cancers and immunosuppressive

PT    disorders by disrupting interactions of the SH (Src homology) 2 and SH3

PT    motifs of Src family kinase proteins.

XX

PS    Claim 3; Page 33; 40pp; English.

XX

CC    The present sequence is a synthetic peptide which has a high affinity for

CC    the src homology 3 (SH3) domain of protein kinases. Protein kinases are

CC    involved in signal transduction pathways, and this peptide can be used to

CC    inhibit these, by disrupting protein-protein interactions, in the

CC    treatment of cancer, particularly hepatocellular carcinoma, cervical

CC    cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-

CC    associated diseases

XX

SQ    Sequence 11 AA;

Query Match                    78.6%;    Score 33;    DB 3;    Length 11;

Best Local Similarity    83.3%;    Pred. No. 2.3e+02;

Matches       5;    Conservative       1;    Mismatches       0;    Indels       0;    Gaps       0;

Qy            2 QPPPLP 7

Db                   :|||||  
                      3 RPPPLP 8

RESULT 16

AAW06845

ID   AAW06845 standard; peptide; 12 AA.

XX

AC   AAW06845;

XX

DT   16-FEB-1997   (first entry)

XX

DE   Peptide binding the Crk-SH3 domain, used to treat cancer.

XX

KW   Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;

KW   diagnosis; antibody; signal transduction; disease; disorder;

KW   intracellular signalling protein.

XX

OS   Synthetic.

XX

PN   WO9621011-A2.

XX

PD   11-JUL-1996.

XX

PF   28-DEC-1995;   95WO-US016979.

XX

PR   30-DEC-1994;   94US-00367070.

XX

PA   (UYRQ ) UNIV ROCKEFELLER.

XX

PI   Hanafusa H,   Knudsen BS,   Feller SM,   Kuriyan J,   Wu X,   Zheng J;

PI   Cowburn D;

XX

DR   WPI; 1996-333986/33.

XX

PT   New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for

PT   the diagnosis and treatment of defects in intracellular signal

PT   transduction, partic. in cancer.

XX

PS   Claim 3; Page 92; 120pp; English.

XX

CC   New peptides or proteins which comprise these peptides, bind to the Crk-

CC   SH3 domain and competitively inhibit the binding of intracellular

CC   signalling proteins. They can be used in the treatment of a disease or

CC   disorder associated with a defect in intracellular signal transduction,

CC   particularly cancer. They can also be used to diagnose such diseases and

CC   disorders. Antibodies raised against these proteins can be used for the

CC   same purposes. The peptides are derived from the Crk-SH3 binding domains

CC   of intracellular signalling proteins. Peptides related to the invention

CC   are described in AAW03149-63 and AAW06842-W06866

XX

SQ   Sequence 12 AA;

Query Match                   78.6%;   Score 33;   DB 2;   Length 12;

Best Local Similarity   83.3%;   Pred. No. 2.5e+02;

Matches   5;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;



Qy            2 QPPPLP 7  
              :|||||  
Db            2 KPPPLP 7

RESULT 17

AAW38072

ID    AAW38072 standard; peptide; 13 AA.

XX

AC    AAW38072;

XX

DT    23-APR-1998    (first entry)

XX

DE    PPPPY motif containing peptide used to bind WW domains.

XX

KW    Peptide recognition unit; WW domain; cell signalling; growth regulation;  
KW    cytoskeleton organisation; targeted drug screening; modulator;  
KW    WW domain interaction; YAP protein; dystrophin.

XX

OS    Synthetic.

XX

PN    WO9737223-A1.

XX

PD    09-OCT-1997.

XX

PF    03-APR-1997;    97WO-US005547.

XX

PR    03-APR-1996;    96US-00630916.

XX

PA    (CYTO-) CYTOGEN CORP.

PA    (UYNC-) UNIV NORTH CAROLINA.

XX

PI    Pirozzi G,    Kay BK,    Fowlkes DM;

XX

DR    WPI; 1997-503234/46.

XX

PT    Identifying cell signalling and growth regulatory polypeptides by  
PT    reaction with multivalent recognition complex - polypeptides are useful  
PT    in targetted drug selection.

XX

PS    Disclosure; Fig 15B; 220pp; English.

XX

CC    Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is found  
CC    in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
CC    containing this residue have been shown to bind the YAP WW domain, but  
CC    not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
CC    AAW38068-92 were biotinylated and complexed with alkaline streptavidin,  
CC    and used in a cross affinity mapping experiment. They were tested for  
CC    their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were  
CC    expressed as glutathione-S-transferase expression proteins. The present  
CC    peptide, derived from WBP-2A, does not bind to the WW domains of the  
CC    novel protein. The WW domain is a small functional domain. Its name is  
CC    derived from the observation that two tryptophan residues, one in the  
CC    amino terminal portion of the WW domain and one in the carboxyl terminal  
CC    portion, are conserved. Most proteins containing WW domains have a  
CC    function involving cell signalling and growth regulation or the  
CC    organisation of the cytoskeleton. Polypeptides containing a WW domain are

CC identified by treating a multivalent recognition unit complex that has  
CC selective binding affinity for a WW domain, with many polypeptides and  
CC identifying those with selective affinity for the complex. Proteins  
CC containing WW domains are used for targeted drug screening, i.e. to  
CC identify potential modulators of specific WW domain interactions  
XX  
SQ Sequence 13 AA;

Query Match 78.6%; Score 33; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
:|||||  
Db 2 VQPPAP 8

#### RESULT 18

ADB49333

ID ADB49333 standard; peptide; 13 AA.

XX

AC ADB49333;

XX

DT 04-DEC-2003 (first entry)

XX

DE Biotinylated WW domain binding peptide #5.

XX

KW WW domain; drug candidate screening; drug discovery; drug modification;

KW drug refinement; immunogen; WW binding protein; WW domain.

XX

OS Unidentified.

XX

PN US2003077577-A1.

XX

PD 24-APR-2003.

XX

PF 28-JUN-2002; 2002US-00185050.

XX

PR 03-APR-1996; 96US-00630916.

PR 03-APR-1997; 97US-00826516.

XX

PA (PIRO/) PIROZZI G.

PA (KAYB/) KAY B K.

PA (FOWL/) FOWLKES D M.

XX

PI Pirozzi G, Kay BK, Fowlkes DM;

XX

DR WPI; 2003-635075/60.

XX

PT Novel purified polypeptide comprising WW domain, useful for drug

PT discovery, modification and refinement, for discovering polypeptides

PT involved in pharmacological activities, or as an immunogen to generate

PT antibodies.

XX

PS Example; Fig 15A; 133pp; English.

XX

CC The invention describes a purified polypeptide (I) comprising a WW domain

CC which has a sequence (S1) selected from 11 sequences fully defined in the  
 CC specification, a sequence (S2) selected from 48 sequences fully defined  
 CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
 CC amino acids fully defined in the specification. (I) is useful for  
 CC screening a potential drug candidate, by allowing (I) to come into  
 CC contact with at least one recognition unit having a selective affinity  
 CC for the WW domain in (I), in the presence of an amount of a potential  
 CC drug candidate, such that (I) and the recognition unit are capable of  
 CC interacting when brought into contact with one another in the absence of  
 CC the drug candidate, and determining the effect, if any, of the presence  
 CC of the amount of the drug candidate on the interaction of (I) with the  
 CC recognition unit. (I) is useful for drug discovery, modification and  
 CC refinement, for discovering polypeptides involved in pharmacological  
 CC activities, or as an immunogen to generate antibodies. This is the amino  
 CC acid sequence of a WW domain binding peptide.

XX

SQ Sequence 13 AA;

Query Match 78.6%; Score 33; DB 7; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 :|||||  
 Db 2 VQPPAP 8

# RESULT 19

AAR60997

ID AAR60997 standard; peptide; 7 AA.

XX

AC AAR60997;

XX

DT 25-MAR-2003 (revised)

DT 14-APR-1995 (first entry)

XX

DE Fragment of the 3BP1 protein that binds to SH3 of Abl kinase.

XX

KW CD4; T cell; surface antigen; receptor; MHC class II antigen;  
 KW protein-tyrosine kinase; p56lck; TcR/CD3 complex; PI 3-kinase;  
 KW PI 4-kinase; lipid kinase; T cell receptor complex; 3BP1; SH3;  
 KW Abl kinase.

XX

OS Synthetic.

XX

PN WO9418832-A1.

XX

PD 01-SEP-1994.

XX

PF 25-FEB-1994; 94WO-US001840.

XX

PR 26-FEB-1993; 93US-00023915.

XX

PA (DAND ) DANA FARBER CANCER INST INC.

XX

PI Rudd CE, Kanteti P, Cantley L;

XX

DR WPI; 1994-293868/36.

XX

PT Method for inhibiting or reducing signal transduction - utilises peptide  
PT or corresp. nucleic acid which decreases association of PI 3- or 4-  
PT kinase with CD4/p56lck.

XX

PS Example; Page 32; 46pp; English.

XX

CC In order for certain T cells to make an optimal response to antigen, it  
CC is necessary for the T cell surface antigen CD4 to couple to the protein-  
CC tyrosine kinase p56lck. (CD4-p56lck is known to associate with and  
CC functionally synergise with the TcR/CD3 complex.) CD4-p56lck complex in T  
CC cells associates with two lipid kinases: PI 3-kinase and PI 4-kinase,  
CC which suggests that these lipid kinases are also involved in  
CC intracellular signalling via the T cell receptor complex. The interaction  
CC of a lipid kinase, such as PI 3-kinase or PI 4- kinase, with CD4-p56lck,  
CC may be blocked by administering a peptide. This peptide may be a fragment  
CC of the cytoplasmic domain of CD4 (eg AAR60987-R60991), a fragment of  
CC p56lck (eg AAR60992, AAR60993), a fragment of PI 3-kinase (eg AAR60994,  
CC AAR60995), or a fragment of PI 4-kinase. Other proline-rich peptides that  
CC bind to SH3 binding sequences can also be used, such as the fragment of  
CC 3BP1 protein that binds to the SH3 of the Abl kinase (AAR60997), or a  
CC sequence found in the SOS protein (AAR60999). (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX

SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|||||

Db 1 PPPLP 5

#### RESULT 20

AAR91752

ID AAR91752 standard; peptide; 7 AA.

XX

AC AAR91752;

XX

DT 14-AUG-1996 (first entry)

XX

DE Prolyl endopeptidase inhibitor peptide #7.

XX

KW Prolyl endopeptidase; PEP; inhibitory peptide; animal feed; therapy;  
KW prevention; dementia; human.

XX

OS Synthetic.

XX

PN JP08059697-A.

XX

PD 05-MAR-1996.

XX

PF 09-MAR-1995; 95JP-00079661.

XX

PR 15-JUN-1994; 94JP-00158031.  
 XX  
 PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
 PA (NIHA-) NIPPON HAM KK.  
 XX  
 DR WPI; 1996-184809/19.  
 XX  
 PT Prolyl:endo:peptidase inhibitory peptide(s) - useful as additives for  
 PT food and animal feed and to treat and prevent dementia.  
 XX  
 PS Claim 1; Page 11; 11pp; Japanese.  
 XX  
 CC AAR91746-R91753 represent prolyl endopeptidase (PEP) inhibitory peptides.  
 CC These peptides are useful as PEP inhibitors in functional foods and in  
 CC animal feeds. They are used to prepare oral and parenteral pharmaceutical  
 CC preparations for the treatment and prevention of dementia of animals,  
 CC including humans. The advantage with using these peptides, is that they  
 CC are safe and easily absorbed  
 XX  
 SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 2 PPPLP 6

# RESULT 21

AAM46827

ID AAM46827 standard; peptide; 7 AA.

XX

AC AAM46827;

XX

DT 25-OCT-2001 (first entry)

XX

DE H11 binding site consensus conforming peptide (CCP) #3098.

XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN CA2290722-A1.

XX

PD 08-JUN-2001.

XX

PF 08-DEC-1999; 99CA-02290722.

XX

PR 08-DEC-1999; 99CA-02290722.

XX

PA (NOVO-) NOVOPHARM BIOTECH INC.

XX

PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, Macdonald GC;

XX

DR WPI; 2001-425937/46.

XX

PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated antigen-  
PT binding fragments of an antibody that binds specifically to the complex.

XX

PS Example 4; Page 112; 154pp; English.

XX

CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention

XX

SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

||||

Db 3 PPPLP 7

RESULT 22

AAM46861

ID AAM46861 standard; peptide; 7 AA.

XX

AC AAM46861;

XX

DT 25-OCT-2001 (first entry)

XX

DE H11 binding site consensus conforming peptide (CCP) #3132.

XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-02290722.  
 XX  
 PR 08-DEC-1999; 99CA-02290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX  
 PS Example 4; Page 112; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

RESULT 23  
 AAM46876  
 ID AAM46876 standard; peptide; 7 AA.  
 XX  
 AC AAM46876;

XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE H11 binding site consensus conforming peptide (CCP) #3147.  
 XX  
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-02290722.  
 XX  
 PR 08-DEC-1999; 99CA-02290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX  
 PS Example 4; Page 112; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy            3 PPPLP 7  
              | | | |  
Db            3 PPPLP 7

RESULT 24

AAM47027

ID    AAM47027 standard; peptide; 7 AA.

XX

AC    AAM47027;

XX

DT    25-OCT-2001    (first entry)

XX

DE    H11 binding site consensus conforming peptide (CCP) #3298.

XX

KW    Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW    immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW    cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW    astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW    ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS    Homo sapiens.

OS    Synthetic.

XX

PN    CA2290722-A1.

XX

PD    08-JUN-2001.

XX

PF    08-DEC-1999;    99CA-02290722.

XX

PR    08-DEC-1999;    99CA-02290722.

XX

PA    (NOVO-) NOVOPHARM BIOTECH INC.

XX

PI    Kaplan HA,    Maiti PK,    Fast DG,    Herman W,    Dan MD,    Lewis KE;

PI    Entwistle JM,    Macdonald GC;

XX

DR    WPI; 2001-425937/46.

XX

PT    Composition useful for treating and diagnosing cancer, comprises stress  
PT    protein-peptide complexes associated with tumor, and isolated antigen-  
PT    binding fragments of an antibody that binds specifically to the complex.

XX

PS    Example 4; Page 112; 154pp; English.

XX

CC    The present invention describes a composition (I) comprising stress  
CC    protein-peptide complexes (SPPC) associated with tumours that is  
CC    specifically immunogenically cross-reactive with cell surface-associated  
CC    SPPCs specific to target cancer (TC). Also described is an isolated  
CC    antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC    or a population of different SPPCs consisting of immunogenic cancer cell  
CC    surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC    used in vaccine production and as a tumour-specific immunogenic response  
CC    inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC    subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC    oligodendroglioma, ependymoma, medulloblastoma, and primitive neural

CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention  
XX  
SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
| | | |  
Db 3 PPPLP 7

RESULT 25

AAM46856

ID AAM46856 standard; peptide; 7 AA.

XX

AC AAM46856;

XX

DT 25-OCT-2001 (first entry)

XX

DE H11 binding site consensus conforming peptide (CCP) #3127.

XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN CA2290722-A1.

XX

PD 08-JUN-2001.

XX

PF 08-DEC-1999; 99CA-02290722.

XX

PR 08-DEC-1999; 99CA-02290722.

XX

PA (NOVO-) NOVOPHARM BIOTECH INC.

XX

PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;

PI Entwistle JM, Macdonald GC;

XX

DR WPI; 2001-425937/46.

XX

PT Composition useful for treating and diagnosing cancer, comprises stress

PT protein-peptide complexes associated with tumor, and isolated antigen-

PT binding fragments of an antibody that binds specifically to the complex.

XX

PS Example 4; Page 112; 154pp; English.

XX

CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention

XX

SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

#### RESULT 26

AAM46871

ID AAM46871 standard; peptide; 7 AA.

XX

AC AAM46871;

XX

DT 25-OCT-2001 (first entry)

XX

DE H11 binding site consensus conforming peptide (CCP) #3142.

XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;

KW immunogenically cross-reactive; cancer; immunogenic cancer cell;

KW cytostatic; vaccine; tumour-specific immunogenic response inducer;

KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;

KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN CA2290722-A1.

XX

PD 08-JUN-2001.

XX

PF 08-DEC-1999; 99CA-02290722.

XX

PR 08-DEC-1999; 99CA-02290722.

XX

PA (NOVO-) NOVOPHARM BIOTECH INC.

XX

PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX  
 PS Example 4; Page 112; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

#### RESULT 27

AAM46851

ID AAM46851 standard; peptide; 7 AA.

XX

AC AAM46851;

XX

DT 25-OCT-2001 (first entry)

XX

DE H11 binding site consensus conforming peptide (CCP) #3122.

XX

KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX

OS Homo sapiens.

OS Synthetic.

XX  
 PN CA2290722-A1.  
 XX  
 PD 08-JUN-2001.  
 XX  
 PF 08-DEC-1999; 99CA-02290722.  
 XX  
 PR 08-DEC-1999; 99CA-02290722.  
 XX  
 PA (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 PI Entwistle JM, Macdonald GC;  
 XX  
 DR WPI; 2001-425937/46.  
 XX  
 PT Composition useful for treating and diagnosing cancer, comprises stress  
 PT protein-peptide complexes associated with tumor, and isolated antigen-  
 PT binding fragments of an antibody that binds specifically to the complex.  
 XX  
 PS Example 4; Page 112; 154pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising stress  
 CC protein-peptide complexes (SPPC) associated with tumours that is  
 CC specifically immunogenically cross-reactive with cell surface-associated  
 CC SPPCs specific to target cancer (TC). Also described is an isolated  
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
 CC or a population of different SPPCs consisting of immunogenic cancer cell  
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 CC used in vaccine production and as a tumour-specific immunogenic response  
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 CC or imaging cancer cells, and to monitor the course of amelioration of  
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
 CC which are used in the exemplification of the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 3 PPPLP 7

RESULT 28  
 AAM46866  
 ID AAM46866 standard; peptide; 7 AA.  
 XX  
 AC AAM46866;  
 XX  
 DT 25-OCT-2001 (first entry)

XX  
DE H11 binding site consensus conforming peptide (CCP) #3137.  
XX  
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;  
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;  
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN CA2290722-A1.  
XX  
PD 08-JUN-2001.  
XX  
PF 08-DEC-1999; 99CA-02290722.  
XX  
PR 08-DEC-1999; 99CA-02290722.  
XX  
PA (NOVO-) NOVOPHARM BIOTECH INC.  
XX  
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
PI Entwistle JM, Macdonald GC;  
XX  
DR WPI; 2001-425937/46.  
XX  
PT Composition useful for treating and diagnosing cancer, comprises stress  
PT protein-peptide complexes associated with tumor, and isolated antigen-  
PT binding fragments of an antibody that binds specifically to the complex.  
XX  
PS Example 4; Page 112; 154pp; English.  
XX  
CC The present invention describes a composition (I) comprising stress  
CC protein-peptide complexes (SPPC) associated with tumours that is  
CC specifically immunogenically cross-reactive with cell surface-associated  
CC SPPCs specific to target cancer (TC). Also described is an isolated  
CC antigen-binding fragment of an antibody that binds specifically to SPPCs  
CC or a population of different SPPCs consisting of immunogenic cancer cell  
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be  
CC used in vaccine production and as a tumour-specific immunogenic response  
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a  
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting  
CC or imaging cancer cells, and to monitor the course of amelioration of  
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides  
CC which are used in the exemplification of the present invention  
XX  
SQ Sequence 7 AA;

Query Match 76.2%; Score 32; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

Db                    |||||  
                      3 PPPLP 7

RESULT 29

AAR71945

ID    AAR71945 standard; peptide; 8 AA.

XX

AC    AAR71945;

XX

DT    25-MAR-2003    (revised)

DT    17-OCT-1995    (first entry)

XX

DE    Human 3BP1 peptide.

XX

KW    Grb3-3; cancer; apoptosis; AIDS; gene therapy; 3BP1; SH3 domain.

XX

OS    Synthetic.

XX

PN    WO9507981-A1.

XX

PD    23-MAR-1995.

XX

PF    09-MAY-1994;    94WO-FR000542.

XX

PR    15-SEP-1993;    93FR-00010971.

XX

PA    (RHON ) RHONE POULENC RORER SA.

XX

PI    Schweighoffer F,    Tocque B;

XX

DR    WPI; 1995-131349/17.

XX

PT    New human Grb3-3 gene and vectors contg. it - useful in control of cell  
PT    death etc. partic. for treating cancer and AIDS.

XX

PS    Example 2; Page 11; 3lpp; French.

XX

CC    The hSOS1 and 3BP1 peptides given in AAR71944-45 were used to demonstrate  
CC    that the newly isolated human Grb3-3 protein was able to bind hSOS1, but  
CC    not to the 3BP1 peptide, which corresponds to the SH3 domain of Abl and  
CC    Src. A Grb3-3G162R mutant was unable to bind the hSOS1 peptide. (Updated  
CC    on 25-MAR-2003 to correct PN field.)

XX

SQ    Sequence 8 AA;

Query Match                    76.2%;    Score 32;    DB 2;    Length 8;

Best Local Similarity    100.0%;    Pred. No. 1.4e+06;

Matches        5;    Conservative        0;    Mismatches        0;    Indels            0;    Gaps            0;

Qy                    3 PPPLP 7

                      |||||

Db                    1 PPPLP 5

RESULT 30

AAR77371

ID AAR77371 standard; peptide; 10 AA.

XX

AC AAR77371;

XX

DT 17-JAN-1996 (first entry)

XX

DE SH3 binding domain 3BP-1.

XX

KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;

KW Src homology 3; SH3 binding domain; 3BP-1.

XX

OS Homo sapiens.

XX

PN WO9525125-A1.

XX

PD 21-SEP-1995.

XX

PF 14-MAR-1995; 95WO-US003610.

XX

PR 14-MAR-1994; 94US-00212190.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kohn EC, Liotta LA, Kim YS;

XX

DR WPI; 1995-336944/43.

XX

PT DNA encoding CAI resistance proteins - used in gene therapy, and for

PT detecting CAI resistance in biological samples.

XX

PS Example 4; Page 40; 56pp; English.

XX

CC CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human  
CC melanoma cells, contains a unique proline-rich sequence which fulfills  
CC the consensus definition for Src homology 3 (SH3) binding proteins  
CC (AAR77366). 4 Unique versions (AAR77367-70) are present that show  
CC homology to the known SH3 binding domains: 3BP-1, and the p85-alpha-1 and  
CC -2 subunits of phosphatidylinositol 3' kinase (AAR77371-73)

XX

SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|||||

Db 5 PPPLP 9

RESULT 31

AAW06861

ID AAW06861 standard; peptide; 10 AA.

XX

AC AAW06861;

XX

DT 16-FEB-1997 (first entry)



XX  
DE Peptide binding the Crk-SH3 domain, used to treat cancer.  
XX  
KW Peptide; binding; inhibition; binding domain; Crk-SH3; cancer; treatment;  
KW diagnosis; antibody; signal transduction; disease; disorder;  
KW intracellular signalling protein.  
XX  
OS Synthetic.  
XX  
PN WO9621011-A2.  
XX  
PD 11-JUL-1996.  
XX  
PF 28-DEC-1995; 95WO-US016979.  
XX  
PR 30-DEC-1994; 94US-00367070.  
XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX  
PI Hanafusa H, Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;  
PI Cowburn D;  
XX  
DR WPI; 1996-333986/33.  
XX  
PT New peptide(s) which bind the Crk-SH3 domain - used to develop prods. for  
PT the diagnosis and treatment of defects in intracellular signal  
PT transduction, partic. in cancer.  
XX  
PS Claim 3; Page 93; 120pp; English.  
XX  
CC New peptides or proteins which comprise these peptides, bind to the Crk-  
CC SH3 domain and competitively inhibit the binding of intracellular  
CC signalling proteins. They can be used in the treatment of a disease or  
CC disorder associated with a defect in intracellular signal transduction,  
CC particularly cancer. They can also be used to diagnose such diseases and  
CC disorders. Antibodies raised against these proteins can be used for the  
CC same purposes. The peptides are derived from the Crk-SH3 binding domains  
CC of intracellular signalling proteins. Peptides related to the invention  
CC are described in AAW03149-63 and AAW06842-W06866  
XX  
SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 2 PPPLP 6

RESULT 32  
AAW38097  
ID AAW38097 standard; peptide; 10 AA.  
XX  
AC AAW38097;  
XX

DT 23-APR-1998 (first entry)  
 XX  
 DE PPPPY motif containing peptide used to bind WW domains.  
 XX  
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;  
 KW cytoskeleton organisation; targeted drug screening; modulator;  
 KW WW domain interaction; YAP protein; dystrophin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9737223-A1.  
 XX  
 PD 09-OCT-1997.  
 XX  
 PF 03-APR-1997; 97WO-US005547.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 XX  
 DR WPI; 1997-503234/46.  
 XX  
 PT Identifying cell signalling and growth regulatory polypeptides by  
 PT reaction with multivalent recognition complex - polypeptides are useful  
 PT in targetted drug selection.  
 XX  
 PS Disclosure; Fig 15D; 220pp; English.  
 XX  
 CC Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is found  
 CC in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides  
 CC containing this residue have been shown to bind the YAP WW domain, but  
 CC not the WW domain from dystrophin or to a panel of SH3 domains. Peptides  
 CC AAW38068-92 were biotinylated and complexed with alkaline streptavidin,  
 CC and used in a cross affinity mapping experiment. They were tested for  
 CC their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were  
 CC expressed as glutathione-S-transferase expression proteins. The present  
 CC peptide, derived from formin, does not bind to the WW domains of the  
 CC novel protein. The WW domain is a small functional domain. Its name is  
 CC derived from the observation that two tryptophan residues, 1 in the amino  
 CC terminal portion of the WW domain and 1 in the carboxyl terminal portion,  
 CC are conserved. Most proteins containing WW domains have a function  
 CC involving cell signalling and growth regulation or the organisation of  
 CC the cytoskeleton. Polypeptides containing a WW domain are identified by  
 CC treating a multivalent recognition unit complex that has selective  
 CC binding affinity for a WW domain, with many polypeptides and identifying  
 CC those with selective affinity for the complex. Proteins containing WW  
 CC domains are used for targeted drug screening, i.e. to identify potential  
 CC modulators of specific WW domain interactions  
 XX  
 SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY            3 PPPLP 7  
              | | | |  
Db            5 PPPLP 9

RESULT 33

AAW38074

ID    AAW38074 standard; peptide; 10 AA.

XX

AC    AAW38074;

XX

DT    23-APR-1998    (first entry)

XX

DE    PPPPY motif containing peptide used to bind WW domains.

XX

KW    Peptide recognition unit; WW domain; cell signalling; growth regulation;

KW    cytoskeleton organisation; targeted drug screening; modulator;

KW    WW domain interaction; YAP protein; dystrophin.

XX

OS    Synthetic.

XX

PN    WO9737223-A1.

XX

PD    09-OCT-1997.

XX

PF    03-APR-1997;    97WO-US005547.

XX

PR    03-APR-1996;    96US-00630916.

XX

PA    (CYTO-) CYTOGEN CORP.

PA    (UYNC-) UNIV NORTH CAROLINA.

XX

PI    Pirozzi G,    Kay BK,    Fowlkes DM;

XX

DR    WPI; 1997-503234/46.

XX

PT    Identifying cell signalling and growth regulatory polypeptides by

PT    reaction with multivalent recognition complex - polypeptides are useful

PT    in targetted drug selection.

XX

PS    Disclosure; Fig 15B; 220pp; English.

XX

CC    Peptides AAW38068-92 contain PPPPY-like motifs. The PPPY motif is found

CC    in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides

CC    containing this residue have been shown to bind the YAP WW domain, but

CC    not the WW domain from dystrophin or to a panel of SH3 domains. Peptides

CC    AAW38068-92 were biotinylated and complexed with alkaline streptavidin,

CC    and used in a cross affinity mapping experiment. They were tested for

CC    their ability to bind to the 3 WW domains of WWP4 (AAW36797), which were

CC    expressed as glutathione-S-transferase expression proteins. The present

CC    peptide, derived from formin, does not bind to the WW domains of the

CC    novel protein. The WW domain is a small functional domain. Its name is

CC    derived from the observation that two tryptophan residues, one in the

CC    amino terminal portion of the WW domain and one in the carboxyl terminal

CC    portion, are conserved. Most proteins containing WW domains have a

CC    function involving cell signalling and growth regulation or the

CC organisation of the cytoskeleton. Polypeptides containing a WW domain are  
CC identified by treating a multivalent recognition unit complex that has  
CC selective binding affinity for a WW domain, with many polypeptides and  
CC identifying those with selective affinity for the complex. Proteins  
CC containing WW domains are used for targeted drug screening, i.e. to  
CC identify potential modulators of specific WW domain interactions

XX

SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

||||

Db 5 PPPLP 9

#### RESULT 34

AAB86131

ID AAB86131 standard; protein; 10 AA.

XX

AC AAB86131;

XX

DT 30-JUL-2001 (first entry)

XX

DE Proline-rich peptide.

XX

KW Transport system; gene therapy; infection; tumor LLO;

KW human immune deficiency virus; hemophilia; muscular dystrophy; capsid;

KW cystic fibrosis; virus-like particle; cell targeting; listeriolysin O.

XX

OS Unidentified.

XX

PN WO200132851-A2.

XX

PD 10-MAY-2001.

XX

PF 03-NOV-2000; 2000WO-EP010876.

XX

PR 03-NOV-1999; 99DE-01052957.

XX

PA (ACGT-) ACGT PROGENOMICS AG.

XX

PI Boehm G, Rudolph R, Schmidt U, Esser D;

XX

DR WPI; 2001-316433/33.

XX

PT Transport system for compounds, useful e.g. in gene therapy, comprises  
PT mosaic-like assembly of different protein subunits able to encapsulate  
PT compounds.

XX

PS Example 11; Page 35; 106pp; German.

XX

CC This invention describes a novel transport system (A) for molecular  
CC substances (I) containing recombinantly prepared subunits (SU) based on  
CC amino acids (aa) comprising: (i) at least two modified SU with one

CC difference; and/or (ii) one or more modified SU with at least two  
 CC differences; and (iii) (optionally) unmodified SU. The various SU are  
 CC combined in a mosaic fashion to form (A) in which (I) can be  
 CC encapsulated. (A) Are used to deliver (I) specifically to cells,  
 CC particularly DNA to eukaryotic cells for gene therapy, e.g. of infections  
 CC by human immune deficiency virus, tumors and a wide range of inherited  
 CC diseases such as hemophilia, muscular dystrophy or cystic fibrosis.  
 CC Capsids or other virus-like particles can be assembled, simply and in  
 CC modular fashion, in vitro, allowing control over stoichiometric  
 CC composition. SU can be modified to impart a wide variety of selected  
 CC properties, e.g. cell targeting, improved cellular uptake and reduced  
 CC immunogenicity. (A) do not require extensive testing to ensure that they  
 CC are safe (contrast replication-deficient viruses), also SU can be  
 CC prepared in very pure form and are easily labeled fluorescently (for  
 CC quality control or localization). This sequence represents a proline-rich  
 CC peptide used in the construction of a a *Listeria monocytogenes*  
 CC listeriolysin LLO variant which is used to illustrate the method of the  
 CC invention

XX

SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 6 PPPLP 10

# RESULT 35

AAB86149

ID AAB86149 standard; peptide; 10 AA.

XX

AC AAB86149;

XX

DT 31-JUL-2001 (first entry)

XX

DE Proline-rich peptide fragment.

XX

KW Packaging; protein shell; transport system; gene therapy; GFP-PPLP;  
 KW icosahedral virus capsid; enhanced green fluorescent protein; eGFP;  
 KW fusion construct; proline-rich.

XX

OS Unidentified.

XX

PN WO200132852-A2.

XX

PD 10-MAY-2001.

XX

PF 03-NOV-2000; 2000WO-EP010878.

XX

PR 03-NOV-1999; 99DE-01052982.

XX

PA (ACGT-) ACGT PROGENOMICS AG.

XX

PI Boehm G, Esser D, Schmidt U;

XX  
 DR WPI; 2001-316434/33.  
 XX  
 PT Packaging compounds in protein shells, useful e.g. in gene therapy, by  
 PT binding a compound to immobilized shell fragment, then releasing it from  
 PT the matrix and assembly into shells.  
 XX  
 PS Example 6; Page 26; 62pp; German.  
 XX  
 CC This invention describes a novel method for packaging molecular  
 CC substances (I) in protein shells which comprises binding a shell fragment  
 CC (II), via a first region, to a matrix (M), then treating bound (II) with  
 CC (I) so that this binds through a second region of (II). The (I)-(II)  
 CC product, or part of it, is separated from M and assembled, with other  
 CC (II), to form the shells. The separation and assembly steps may be  
 CC performed in either sequence. Packaging of (I) is used to prepare  
 CC transport systems for genes or active agents, particularly in gene  
 CC therapy. The process provides very efficient packaging of (I), including  
 CC compounds that aggregate in solution or have other unfavorable  
 CC properties. Even very long DNA can be packaged, when combined with a  
 CC condensing agent, and the method is applicable to any sort of protein  
 CC shell, not just icosahedral virus capsids. The integrated (II) can be  
 CC screened for optimization of its packaging properties. e.g. maximum size  
 CC of (I) that can be accommodated. This sequence represents a proline-rich  
 CC peptide fragment used in the production of the fusion construct  
 CC comprising the Aequorea victoria enhanced green fluorescent protein  
 CC (eGFP) and a proline rich region which is used to illustrate the method  
 CC of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 6 PPPLP 10

# RESULT 36

AAB70933

ID AAB70933 standard; protein; 10 AA.

XX

AC AAB70933;

XX

DT 30-JUL-2001 (first entry)

XX

DE Polyoma virus VP1 variant PyVP1-WW150 proline-rich fragment.

XX

KW VP1; coat protein; WW domain; proline-rich; immobilization; biosensor;  
 KW bioreactor; protein packaging; PyVP1-WW150.

XX

OS Polyoma virus.

XX

PN WO200132684-A2.

XX

PD 10-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000WO-EP010873.  
 XX  
 PR 03-NOV-1999; 99DE-01052956.  
 XX  
 PA (ACGT-) ACGT PROGENOMICS AG.  
 XX  
 PI Boehm G, Schmidt U, Parthier C, Guenther C;  
 XX  
 DR WPI; 2001-343471/36.  
 XX  
 PT Linking two or more molecules through adapter sequences, useful e.g. for  
 PT purifying recombinant proteins, by exploiting interaction between WW  
 PT domain and proline-rich sequence.  
 XX  
 PS Example 5; Page 26; 100pp; German.  
 XX  
 CC This invention describes a novel method (M1) for linking two or more  
 CC molecular substances (A) together via adapter sequences (AS). One (A) is  
 CC modified so that it contains, as AS, a WW domain or derived structure in  
 CC at least one region, and a second (A) is modified so that it contains, as  
 CC AS, a proline-rich sequence (PRS) able to bind to WW domain or its  
 CC derivative in at least one region and the modified components are allowed  
 CC to interact together through WW and PRS. The method is used to provide  
 CC permanent or temporary association between (A), e.g. temporary  
 CC immobilization, and matrix-assisted refolding, of recombinant proteins  
 CC from crude cell extracts or permanent immobilization in biosensors or  
 CC bioreactors, for directing packaging of proteins inside a virus-like  
 CC shell, or production of chimeric proteins (e.g. bispecific antibodies),  
 CC for medical, therapeutic, diagnostic or biotechnological use. Interaction  
 CC between WW and PRS is very strong (dissociation constant 20-100 nM) but  
 CC only temporary, and can be stabilized (e.g. against extremes of salt  
 CC concentration or temperature) by formation of disulfide bridges. Compared  
 CC with other systems with comparable properties, the WW/PRS system is  
 CC exceptionally small and compact and for many applications, e.g. antibody-  
 CC antigen interaction, is clearly superior to other ligand binding domains.  
 CC The system can only produce heterodimers. This sequence represents a  
 CC proline-rich fragment of the Polyoma virus coat protein VP1 variant PyVP1  
 CC -WW150 construct which is used to illustrate the method of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 | | | | |  
 Db 6 PPPLP 10

RESULT 37  
 ADB49372  
 ID ADB49372 standard; peptide; 10 AA.  
 XX  
 AC ADB49372;

XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Biotinylated WW domain binding peptide #30.  
 XX  
 KW WW domain; drug candidate screening; drug discovery; drug modification;  
 KW drug refinement; immunogen; WW binding protein; WW domain.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003077577-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 28-JUN-2002; 2002US-00185050.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 PR 03-APR-1997; 97US-00826516.  
 XX  
 PA (PIRO/) PIROZZI G.  
 PA (KAYB/) KAY B K.  
 PA (FOWL/) FOWLKES D M.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM;  
 XX  
 DR WPI; 2003-635075/60.  
 XX  
 PT Novel purified polypeptide comprising WW domain, useful for drug  
 PT discovery, modification and refinement, for discovering polypeptides  
 PT involved in pharmacological activities, or as an immunogen to generate  
 PT antibodies.  
 XX  
 PS Example; Fig 15C; 133pp; English.  
 XX  
 CC The invention describes a purified polypeptide (I) comprising a WW domain  
 CC which has a sequence (S1) selected from 11 sequences fully defined in the  
 CC specification, a sequence (S2) selected from 48 sequences fully defined  
 CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
 CC amino acids fully defined in the specification. (I) is useful for  
 CC screening a potential drug candidate, by allowing (I) to come into  
 CC contact with at least one recognition unit having a selective affinity  
 CC for the WW domain in (I), in the presence of an amount of a potential  
 CC drug candidate, such that (I) and the recognition unit are capable of  
 CC interacting when brought into contact with one another in the absence of  
 CC the drug candidate, and determining the effect, if any, of the presence  
 CC of the amount of the drug candidate on the interaction of (I) with the  
 CC recognition unit. (I) is useful for drug discovery, modification and  
 CC refinement, for discovering polypeptides involved in pharmacological  
 CC activities, or as an immunogen to generate antibodies. This is the amino  
 CC acid sequence of a WW domain binding peptide.  
 XX  
 SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy            3 PPPLP 7  
              |||||  
Db            5 PPPLP 9

RESULT 38

ADB49335

ID    ADB49335 standard; peptide; 10 AA.

XX

AC    ADB49335;

XX

DT    04-DEC-2003    (first entry)

XX

DE    Biotinylated WW domain binding peptide #7.

XX

KW    WW domain; drug candidate screening; drug discovery; drug modification;

KW    drug refinement; immunogen; WW binding protein; WW domain.

XX

OS    Unidentified.

XX

PN    US2003077577-A1.

XX

PD    24-APR-2003.

XX

PF    28-JUN-2002; 2002US-00185050.

XX

PR    03-APR-1996;    96US-00630916.

PR    03-APR-1997;    97US-00826516.

XX

PA    (PIRO/) PIROZZI G.

PA    (KAYB/) KAY B K.

PA    (FOWL/) FOWLKES D M.

XX

PI    Pirozzi G,    Kay BK,    Fowlkes DM;

XX

DR    WPI; 2003-635075/60.

XX

PT    Novel purified polypeptide comprising WW domain, useful for drug

PT    discovery, modification and refinement, for discovering polypeptides

PT    involved in pharmacological activities, or as an immunogen to generate

PT    antibodies.

XX

PS    Example; Fig 15A; 133pp; English.

XX

CC    The invention describes a purified polypeptide (I) comprising a WW domain

CC    which has a sequence (S1) selected from 11 sequences fully defined in the

CC    specification, a sequence (S2) selected from 48 sequences fully defined

CC    in the specification or a sequence (S3) comprising 683, 906, 224 or 725

CC    amino acids fully defined in the specification. (I) is useful for

CC    screening a potential drug candidate, by allowing (I) to come into

CC    contact with at least one recognition unit having a selective affinity

CC    for the WW domain in (I), in the presence of an amount of a potential

CC    drug candidate, such that (I) and the recognition unit are capable of

CC    interacting when brought into contact with one another in the absence of

CC    the drug candidate, and determining the effect, if any, of the presence

CC    of the amount of the drug candidate on the interaction of (I) with the

CC    recognition unit. (I) is useful for drug discovery, modification and

CC refinement, for discovering polypeptides involved in pharmacological  
CC activities, or as an immunogen to generate antibodies. This is the amino  
CC acid sequence of a WW domain binding peptide.

XX

SQ Sequence 10 AA;

Query Match 76.2%; Score 32; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

|||||

Db 5 PPPLP 9

RESULT 39

AAB21129

ID AAB21129 standard; peptide; 11 AA.

XX

AC AAB21129;

XX

DT 19-JAN-2001 (first entry)

XX

DE Src homology 3 domain binding peptide #6.

XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;

KW signal transduction inhibition; immune suppression-associated disease.

XX

OS Synthetic.

XX

PN WO200047607-A1.

XX

PD 17-AUG-2000.

XX

PF 12-FEB-2000; 2000WO-KR000107.

XX

PR 12-FEB-1999; 99AU-00008643.

PR 02-JUN-1999; 99KR-00020282.

XX

PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX

PI Yoon JH, Han YT, Lee KY;

XX

DR WPI; 2000-533010/48.

XX

PT Synthetic peptides useful for treating cancers and immunosuppressive

PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3

PT motifs of Src family kinase proteins.

XX

PS Claim 3; Page 34; 40pp; English.

XX

CC The present sequence is a synthetic peptide which has a high affinity for  
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are  
CC involved in signal transduction pathways, and this peptide can be used to  
CC inhibit these, by disrupting protein-protein interactions, in the  
CC treatment of cancer, particularly hepatocellular carcinoma, cervical

CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-  
CC associated diseases

XX

SQ Sequence 11 AA;

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

||||

Db 4 PPPLP 8

RESULT 40

AAB21132

ID AAB21132 standard; peptide; 11 AA.

XX

AC AAB21132;

XX

DT 19-JAN-2001 (first entry)

XX

DE Src homology 3 domain binding peptide #9.

XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;

KW signal transduction inhibition; immune suppression-associated disease.

XX

OS Synthetic.

XX

PN WO200047607-A1.

XX

PD 17-AUG-2000.

XX

PF 12-FEB-2000; 2000WO-KR000107.

XX

PR 12-FEB-1999; 99AU-00008643.

PR 02-JUN-1999; 99KR-00020282.

XX

PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX

PI Yoon JH, Han YT, Lee KY;

XX

DR WPI; 2000-533010/48.

XX

PT Synthetic peptides useful for treating cancers and immunosuppressive

PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3

PT motifs of Src family kinase proteins.

XX

PS Claim 3; Page 35; 40pp; English.

XX

CC The present sequence is a synthetic peptide which has a high affinity for

CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are

CC involved in signal transduction pathways, and this peptide can be used to

CC inhibit these, by disrupting protein-protein interactions, in the

CC treatment of cancer, particularly hepatocellular carcinoma, cervical

CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-

CC associated diseases

XX

SQ Sequence 11 AA;

Query Match 76.2%; Score 32; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|||||

Db 4 PPPLP 8

#### RESULT 41

AAB21126

ID AAB21126 standard; peptide; 11 AA.

XX

AC AAB21126;

XX

DT 19-JAN-2001 (first entry)

XX

DE Src homology 3 domain binding peptide #3.

XX

KW Src homology domain 3; SH3; protein-protein interaction; cancer;

KW signal transduction inhibition; immune suppression-associated disease.

XX

OS Synthetic.

XX

PN WO200047607-A1.

XX

PD 17-AUG-2000.

XX

PF 12-FEB-2000; 2000WO-KR000107.

XX

PR 12-FEB-1999; 99AU-00008643.

PR 02-JUN-1999; 99KR-00020282.

XX

PA (YOON/) YOON J H.

PA (HANY/) HAN Y T.

XX

PI Yoon JH, Han YT, Lee KY;

XX

DR WPI; 2000-533010/48.

XX

PT Synthetic peptides useful for treating cancers and immunosuppressive

PT disorders by disrupting interactions of the SH (Src homology) 2 and SH3

PT motifs of Src family kinase proteins.

XX

PS Claim 3; Page 33; 40pp; English.

XX

CC The present sequence is a synthetic peptide which has a high affinity for  
CC the src homology 3 (SH3) domain of protein kinases. Protein kinases are  
CC involved in signal transduction pathways, and this peptide can be used to  
CC inhibit these, by disrupting protein-protein interactions, in the  
CC treatment of cancer, particularly hepatocellular carcinoma, cervical  
CC cancer, colon adenocarcinoma and fibrosarcoma, and immune suppression-  
CC associated diseases

XX

SQ Sequence 11 AA;

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

||||

Db 4 PPPLP 8

RESULT 42

ABB99165

ID ABB99165 standard; peptide; 11 AA.

XX

AC ABB99165;

XX

DT 22-NOV-2002 (first entry)

XX

DE Formin-2 FH1 domain repeated proline motif.

XX

KW Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;

KW spontaneous abortion; miscarriage; FH1; proline motif.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /label= Met, Val

XX

PN US2002098489-A1.

XX

PD 25-JUL-2002.

XX

PF 12-APR-2001; 2001US-00835232.

XX

PR 13-APR-2000; 2000US-0196811P.

XX

PA (LEDE/) LEDER P.

PA (LEAD/) LEADER B.

XX

PI Leder P, Leader B;

XX

DR WPI; 2002-690474/74.

XX

PT Determining whether patient has increased risk for recurrent pregnancy  
PT loss by determining whether formin-2 (Fmn-2) gene of patient has  
PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression  
PT in patient.

XX

PS Example 1; Page 7; 137pp; English.

XX

CC The invention relates to a novel method for determining whether a patient  
CC has an increased risk for recurrent pregnancy loss, involving determining  
CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The  
CC method of the invention is useful for determining whether a patient has a

CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous  
CC abortion/miscarriage). The sequence represents a proline motif which is  
CC repeated 11 times in tandem in the FH1 domain of formin-2  
XX  
SQ Sequence 11 AA;

Query Match 76.2%; Score 32; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 6 PPPLP 10

RESULT 43

ABB99166

ID ABB99166 standard; peptide; 11 AA.

XX

AC ABB99166;

XX

DT 22-NOV-2002 (first entry)

XX

DE Formin-2 FH1 domain repeated proline motif #2.

XX

KW Formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;

KW spontaneous abortion; miscarriage; FH1; proline motif.

XX

OS Unidentified.

XX

PN US2002098489-A1.

XX

PD 25-JUL-2002.

XX

PF 12-APR-2001; 2001US-00835232.

XX

PR 13-APR-2000; 2000US-0196811P.

XX

PA (LEDE/) LEDER P.

PA (LEAD/) LEADER B.

XX

PI Leder P, Leader B;

XX

DR WPI; 2002-690474/74.

XX

PT Determining whether patient has increased risk for recurrent pregnancy  
PT loss by determining whether formin-2 (Fmn-2) gene of patient has  
PT mutation, or by measuring Fmn-2 biological activity or Fmn-2 expression  
PT in patient.

XX

PS Example 1; Page 7; 137pp; English.

XX

CC The invention relates to a novel method for determining whether a patient  
CC has an increased risk for recurrent pregnancy loss, involving determining  
CC whether the formin-2 (Fmn-2) gene of the patient has a mutation. The  
CC method of the invention is useful for determining whether a patient has a  
CC increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous

CC abortion/misc.  
CC repeated in t.  
CC invention  
XX  
SQ Sequence 11 A

Query Match  
Best Local Simil.  
Matches 5; C

Qy 3 PPPL  
||||  
Db 7 PPPL

RESULT 44

AAW03154

ID AAW03154 stan

XX

AC AAW03154;

XX

DT 16-FEB-1997

XX

DE Potential Crk

XX

KW Peptide; bind

KW diagnosis; an

KW intracellular

XX

OS Synthetic.

XX

PN WO9621011-A2.

XX

PD 11-JUL-1996.

XX

PF 28-DEC-1995;

XX

PR 30-DEC-1994;

XX

PA (UYRQ ) UNIV

XX

PI Hanafusa H,

PI Cowburn D;

XX

DR WPI; 1996-333

XX

PT New peptide(s

PT the diagnosis

PT transduction,

XX

PS Disclosure; P.

XX

CC New peptides

CC SH3 domain an

CC signalling pr

CC disorder asso

CC particularly

95WO-US016979.

94US-00367070.

ROCKEFELLER.

Knudsen BS, Feller SM, Kuriyan J, Wu X, Zheng J;

986/33.

) which bind the Crk-SH3 domain - used to develop prods. for  
and treatment of defects in intracellular signal  
partic. in cancer.

age 53; 120pp; English.

or proteins which comprise these peptides, bind to the Crk-  
d competitively inhibit the binding of intracellular  
oteins. They can be used in the treatment of a disease or  
ciated with a defect in intracellular signal transduction,  
cancer. They can also be used to diagnose such diseases and

arriage). The sequence represents a proline motif which is  
he FH1 domain of formin-2 in the brain clones of the

A;

76.2%; Score 32; DB 5; Length 11;  
arity 100.0%; Pred. No. 3.2e+02;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;

P 7  
|  
P 11

dard; peptide; 12 AA.

(first entry)

-SH3 binding sequence of protein mSos2/P1.

ing; inhibition; binding domain; Crk-SH3; cancer; treatment;  
tibody; signal transduction; disease; disorder;



CC disorders. Antibodies raised against these proteins can be used for the  
CC same purposes. The peptides are derived from the Crk-SH3 binding domains  
CC of intracellular signalling proteins. Peptides related to the invention  
CC are described in AAW03149-63 and AAW06842-W06866

XX

SQ Sequence 12 AA;

Query Match 76.2%; Score 32; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|||||

Db 3 PPPLP 7

#### RESULT 45

AAW05101

ID AAW05101 standard; peptide; 12 AA.

XX

AC AAW05101;

XX

DT 25-MAR-2003 (revised)

DT 17-DEC-1996 (first entry)

XX

DE Proline-rich SH3 binding peptide pL35.

XX

KW Src homology domain; SH3 domain; oncogene; consensus; lambda 35;

KW random display library.

XX

OS Synthetic.

XX

PN US5541109-A.

XX

PD 30-JUL-1996.

XX

PF 19-APR-1994; 94US-00230047.

XX

PR 19-APR-1994; 94US-00230047.

XX

PA (RHON ) RHONE POULENC RORER PHARM INC.

XX

PI Ivashchenko YD, Ricca GA, Cheadle C, South VJ, Jaye MC;

PI French SM, Searfoss GH;

XX

DR WPI; 1996-361965/36.

XX

PT New DNA encoding proteins that bind to Src-homology domain 3 - used to  
PT inhibit signal transduction, e.g. in cases of T cell activation.

XX

PS Example 1; Col 16; 39pp; English.

XX

CC A fusion protein of glutathione-S-transferase, protein kinase A and Src  
CC SH3 domain was used to screen a mouse embryonal cDNA library in lambda  
CC EXlox. Three positive clones were identified and were designated L17, L14  
CC and L35. The insert from clone L35 encodes a protein which contains a  
CC proline-rich, putative SH3-binding sequence. The present peptide sequence

CC is derived from the putative SH3-binding site (i.e. residues 13-24 of  
CC L35) and was used in an assay to determine binding to the SH3 domains of  
CC c-src and other proteins. (Updated on 25-MAR-2003 to correct PI field.)  
XX  
SQ Sequence 12 AA;

Query Match 76.2%; Score 32; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 4 PPPLP 8

RESULT 46

AAW25457

ID AAW25457 standard; peptide; 12 AA.

XX

AC AAW25457;

XX

DT 27-MAR-1998 (first entry)

XX

DE SH3 domain binding responsible peptide SEQ ID NO:251.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck; Abl;

KW PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

OS Unidentified.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US002298.

XX

PR 16-FEB-1996; 96US-00602999.

XX

PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX

PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JE;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.

XX

PS Claim 21; Page 85; 131pp; English.

XX

CC The present sequence represents a peptide responsible for Src homology

CC region 3 (SH3) binding. SH3 binding peptides are selected from: (a)

CC peptides which bind the SH3 domain of Cortactin; (b) peptides which bind

CC the middle SH3 domain of Nck; (c) peptides which bind the SH3 domain of  
 CC Abl; (d) peptides which bind the SH3 domain of Src; (e) peptides which  
 CC bind the SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain  
 CC of p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding peptides  
 CC can be used in the method to identify inhibitors of their binding to  
 CC their respective SH3 domains, which could be used to modulate the  
 CC pharmacological activity of proteins or polypeptide containing the SH3  
 CC domain. The peptides can also be used to activate Src or Src-related  
 CC protein tyrosine kinases, to stimulate the immune response by increasing  
 CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
 CC and interleukin-1, or to deliver a conjugated molecule to certain  
 CC cellular compartments containing Src or Src related proteins

XX

SQ Sequence 12 AA;

Query Match 76.2%; Score 32; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 6 PPPLP 10

#### RESULT 47

AAB18002

ID AAB18002 standard; peptide; 12 AA.

XX

AC AAB18002;

XX

DT 31-OCT-2000 (first entry)

XX

DE Fc-TNF alpha peptide sequence SEQ ID NO:1116.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
 KW thrombosis; pharmaceutical.

XX

OS Synthetic.

XX

PN WO200024782-A2.

XX

PD 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US025044.

XX

PR 23-OCT-1998; 98US-0105371P.

PR 22-OCT-1999; 99US-00428082.

XX

PA (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheetham J, Boone TC;

XX

DR WPI; 2000-350702/30.

XX

PT Novel composition of matter comprising an Fc domain and pharmacologically  
PT active peptides, useful for treating cancer and autoimmune diseases.

XX

PS Disclosure; Page 604; 608pp; English.

XX

CC The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-  
CC (L2)d-P2-(L3)e-P<sup>3</sup>, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,  
CC P3, and P4 = are each independently sequences of pharmacologically active  
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,  
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host  
CC cells from the present invention can be used for producing pharmaceutical  
CC compositions. The compositions are useful for treating cancer, asthma,  
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
CC a Fab domain) can provide a longer half-life or incorporate functions  
CC such as Fc receptor binding, protein A binding, complement fixation, and  
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to  
CC AAB18003 represent nucleotide and amino acid sequences used in the  
CC exemplification of the present invention

XX

SQ Sequence 12 AA;

Query Match 76.2%; Score 32; DB 3; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7

|||||

Db 8 PPPLP 12

RESULT 48

ADA50131

ID ADA50131 standard; peptide; 12 AA.

XX

AC ADA50131;

XX

DT 20-NOV-2003 (first entry)

XX

DE Mad2 binding peptide (MBP) Seq ID9 amino acid sequence.

XX

KW mitotic checkpoint protein; Mad2; Mad2 binding peptide; MBP;

KW spindle assembly checkpoint; malignant transformation; tumorigenesis;

KW checkpoint protein; breast cancer; cancer; anticancer; cytostatic;

KW prostate cancer; breast cancer; lung cancer; brain cancer; liver cancer;

KW pancreatic cancer; stomach cancer; colon cancer; ovarian cancer;

KW testicular cancer; head and neck cancer; throat cancer;

KW oesophageal cancer; phage display.

XX

OS Synthetic.  
 XX  
 PN US2003083261-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 30-APR-2001; 2001US-00845612.  
 XX  
 PR 30-APR-2001; 2001US-00845612.  
 XX  
 PA (YUHH/) YU H.  
 PA (TANG/) TANG Z.  
 PA (LUOX/) LUO X.  
 PA (RIZO/) RIZO-REY J.  
 XX  
 PI Yu H, Tang Z, Luo X, Rizo-Rey J;  
 XX  
 DR WPI; 2003-616086/58.  
 XX  
 PT Inhibiting Mad2 function, useful for treating cancer, e.g. prostate,  
 PT breast, lung, brain, liver, pancreatic, stomach, colon, ovarian,  
 PT testicular, head or neck cancer comprises contacting a Mad2 protein with  
 PT a peptide that binds Mad2.  
 XX  
 PS Example 4; Fig 1b; 43pp; English.  
 XX  
 CC This invention relates to methods of inhibiting the function of a mitotic  
 CC checkpoint protein, Mad2, using peptides that bind to Mad2. These  
 CC peptides were named Mad2 binding peptides (MBPs). It has been suggested  
 CC that defects of the spindle assembly checkpoint, of which Mad2 is a  
 CC component, contributes to malignant transformation and tumourigenesis.  
 CC Therefore the genes for checkpoint proteins may be involved in the  
 CC pathogenesis of, for example, breast cancer. The MBPs of the invention  
 CC may be used to inhibit Mad2 function and, as a result, these peptides may  
 CC be useful for treating cancer in a subject or screening for anticancer  
 CC agents. Hence the MBPs may have a cytostatic activity. The methods and  
 CC proteins of the invention may be particularly useful for treating cancer  
 CC of, for example, the prostate, breast, lung, brain, liver, pancreatic,  
 CC stomach, colon, ovarian, testicular, head and neck, throat or oesophagus.  
 CC The present sequence is the amino acid sequence of a Mad2 binding peptide  
 CC (MBP) of the invention, which was identified using phage display of  
 CC synthetic peptides in the examples of the specification.  
 XX  
 SQ Sequence 12 AA;

Query Match 76.2%; Score 32; DB 6; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
 :|||||  
 Db 5 LQPPPL 10

RESULT 49  
 AAR84641  
 ID AAR84641 standard; peptide; 13 AA.

XX  
 AC AAR84641;  
 XX  
 DT 26-MAR-1996 (first entry)  
 XX  
 DE Grb2-SOS binding blocking peptide.  
 XX  
 KW SOS; Grb2; BCR-ABL; tyrosine kinase; transformation; Ras; oncoprotein;  
 KW leukaemia; Ras guanine nucleotide releasing protein.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2113494-A.  
 XX  
 PD 15-JUL-1995.  
 XX  
 PF 14-JAN-1994; 94CA-02113494.  
 XX  
 PR 14-JAN-1994; 94CA-02113494.  
 XX  
 PA (MOUN ) MOUNT SINAI HOSPITAL CORP.  
 PA (TEXA ) UNIV TEXAS.  
 XX  
 PI Puil L, Pawson A, Arlinghaus R, Gish G, Liu J;  
 XX  
 DR WPI; 1995-302931/40.  
 XX  
 PT Detection of agents that modify BCR-ABL mediated transformation - useful  
 PT in treatment of leukaemia and other malignancies.  
 XX  
 PS Disclosure; Page 15; 106pp; English.  
 XX  
 CC Peptides (AAR84640-48) that block the binding of Grb2 (AAR84636) to SOS  
 CC Ras guanine nucleotide releasing protein are modelled on the proline-rich  
 CC motifs in the C-terminal region of mouse SOS1 (AAR84638) and SOS2  
 CC (AAR84639). The peptides can be used to screen for compounds that affect  
 CC BCL-ABL mediated transformation. Such compounds have value in the  
 CC treatment of chronic, acute myelogenous or acute lymphocytic leukaemia  
 XX  
 SQ Sequence 13 AA;

Query Match 76.2%; Score 32; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 5 PPPLP 9

RESULT 50  
 AAB70928  
 ID AAB70928 standard; protein; 13 AA.  
 XX  
 AC AAB70928;  
 XX  
 DT 30-JUL-2001 (first entry)

XX  
 DE Polyoma virus VP1 variant proline-rich peptide fragment.  
 XX  
 KW VP1; coat protein; WW domain; proline-rich; immobilization; biosensor;  
 KW bioreactor; protein packaging; PyVP1-WW150-D8C.  
 XX  
 OS Polyoma virus.  
 XX  
 PN WO200132684-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000WO-EP010873.  
 XX  
 PR 03-NOV-1999; 99DE-01052956.  
 XX  
 PA (ACGT-) ACGT PROGENOMICS AG.  
 XX  
 PI Boehm G, Schmidt U, Parthier C, Guenther C;  
 XX  
 DR WPI; 2001-343471/36.  
 XX  
 PT Linking two or more molecules through adapter sequences, useful e.g. for  
 PT purifying recombinant proteins, by exploiting interaction between WW  
 PT domain and proline-rich sequence.  
 XX  
 PS Example 5; Page 88; 100pp; German.  
 XX  
 CC This invention describes a novel method (M1) for linking two or more  
 CC molecular substances (A) together via adapter sequences (AS). One (A) is  
 CC modified so that it contains, as AS, a WW domain or derived structure in  
 CC at least one region, and a second (A) is modified so that it contains, as  
 CC AS, a proline-rich sequence (PRS) able to bind to WW domain or its  
 CC derivative in at least one region and the modified components are allowed  
 CC to interact together through WW and PRS. The method is used to provide  
 CC permanent or temporary association between (A), e.g. temporary  
 CC immobilization, and matrix-assisted refolding, of recombinant proteins  
 CC from crude cell extracts or permanent immobilization in biosensors or  
 CC bioreactors, for directing packaging of proteins inside a virus-like  
 CC shell, or production of chimeric proteins (e.g. bispecific antibodies),  
 CC for medical, therapeutic, diagnostic or biotechnological use. Interaction  
 CC between WW and PRS is very strong (dissociation constant 20-100 nM) but  
 CC only temporary, and can be stabilized (e.g. against extremes of salt  
 CC concentration or temperature) by formation of disulfide bridges. Compared  
 CC with other systems with comparable properties, the WW/PRS system is  
 CC exceptionally small and compact and for many applications, e.g. antibody-  
 CC antigen interaction, is clearly superior to other ligand binding domains.  
 CC The system can only produce heterodimers. This sequence represents a  
 CC proline-rich peptide fragment from Polyoma virus coat protein VP1 which  
 CC is used to illustrate the method of the invention  
 XX  
 SQ Sequence 13 AA;

Query Match 76.2%; Score 32; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            3 PPPLP 7  
              | | | |  
Db            9 PPPLP 13

Search completed: July 4, 2004, 04:40:31  
Job time : 19.403 secs



OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 4.38806 Seconds  
(without alignments)  
82.356 Million cell updates/sec

Title: US-09-641-802-1  
Perfect score: 42  
Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	42	100.0	7	4	US-09-641-803-1	Sequence 1, Appli
2	33	78.6	10	3	US-08-602-999A-278	Sequence 278, App
3	33	78.6	10	4	US-09-500-124-278	Sequence 278, App
4	32	76.2	7	1	US-08-230-047-40	Sequence 40, Appl
5	32	76.2	7	5	PCT-US94-01840-11	Sequence 11, Appl
6	32	76.2	8	1	US-09-641-640-8	Sequence 8, Appli
7	32	76.2	8	2	US-08-612-857-8	Sequence 8, Appli
8	32	76.2	10	1	US-08-230-047-12	Sequence 12, Appl
9	32	76.2	10	1	US-08-230-047-14	Sequence 14, Appl
10	32	76.2	10	1	US-08-212-190A-8	Sequence 8, Appli
11	32	76.2	10	2	US-08-900-321-8	Sequence 8, Appli

12	32	76.2	10	3	US-08-899-595-8	Sequence 8, Appli
13	32	76.2	10	5	PCT-US95-03610-8	Sequence 8, Appli
14	32	76.2	11	1	US-08-336-343A-25	Sequence 25, Appl
15	32	76.2	11	3	US-08-652-877-22	Sequence 22, Appl
16	32	76.2	11	3	US-08-652-877-32	Sequence 32, Appl
17	32	76.2	11	3	US-08-476-515A-22	Sequence 22, Appl
18	32	76.2	11	3	US-08-476-515A-32	Sequence 32, Appl
19	32	76.2	12	1	US-08-230-047-17	Sequence 17, Appl
20	32	76.2	12	3	US-08-602-999A-251	Sequence 251, App
21	32	76.2	12	3	US-08-602-999A-267	Sequence 267, App
22	32	76.2	12	4	US-09-500-124-251	Sequence 251, App
23	32	76.2	12	4	US-09-500-124-267	Sequence 267, App
24	32	76.2	13	4	US-09-845-917A-13	Sequence 13, Appl
25	32	76.2	13	4	US-09-845-917A-14	Sequence 14, Appl
26	32	76.2	13	4	US-09-845-917A-19	Sequence 19, Appl
27	32	76.2	13	4	US-09-845-917A-21	Sequence 21, Appl
28	32	76.2	14	1	US-08-185-432-12	Sequence 12, Appl
29	32	76.2	14	3	US-08-630-916A-63	Sequence 63, Appl
30	32	76.2	14	4	US-08-630-915A-186	Sequence 186, App
31	32	76.2	15	1	US-08-185-432-10	Sequence 10, Appl
32	32	76.2	15	2	US-08-769-745-31	Sequence 31, Appl
33	32	76.2	15	3	US-08-602-999A-356	Sequence 356, App
34	32	76.2	15	3	US-08-602-999A-385	Sequence 385, App
35	32	76.2	15	3	US-08-602-999A-404	Sequence 404, App
36	32	76.2	15	3	US-08-602-999A-414	Sequence 414, App
37	32	76.2	15	3	US-08-602-999A-435	Sequence 435, App
38	32	76.2	15	3	US-08-602-999A-436	Sequence 436, App
39	32	76.2	15	3	US-08-602-999A-441	Sequence 441, App
40	32	76.2	15	3	US-08-602-999A-452	Sequence 452, App
41	32	76.2	15	4	US-09-500-124-356	Sequence 356, App
42	32	76.2	15	4	US-09-500-124-385	Sequence 385, App
43	32	76.2	15	4	US-09-500-124-404	Sequence 404, App
44	32	76.2	15	4	US-09-500-124-414	Sequence 414, App
45	32	76.2	15	4	US-09-500-124-435	Sequence 435, App
46	32	76.2	15	4	US-09-500-124-436	Sequence 436, App
47	32	76.2	15	4	US-09-500-124-441	Sequence 441, App
48	32	76.2	15	4	US-09-500-124-452	Sequence 452, App
49	32	76.2	16	1	US-08-185-432-9	Sequence 9, Appli
50	32	76.2	16	1	US-08-185-432-14	Sequence 14, Appl
51	32	76.2	16	3	US-08-602-999A-197	Sequence 197, App
52	32	76.2	16	4	US-09-500-124-197	Sequence 197, App
53	32	76.2	17	1	US-08-230-047-10	Sequence 10, Appl
54	32	76.2	17	3	US-08-602-999A-360	Sequence 360, App
55	32	76.2	17	3	US-08-602-999A-374	Sequence 374, App
56	32	76.2	17	4	US-09-500-124-360	Sequence 360, App
57	32	76.2	17	4	US-09-500-124-374	Sequence 374, App
58	32	76.2	18	3	US-08-602-999A-320	Sequence 320, App
59	32	76.2	18	3	US-08-602-999A-409	Sequence 409, App
60	32	76.2	18	4	US-09-500-124-320	Sequence 320, App
61	32	76.2	18	4	US-09-500-124-409	Sequence 409, App
62	31	73.8	12	4	US-09-315-926A-16	Sequence 16, Appl
63	31	73.8	13	3	US-08-630-916A-8	Sequence 8, Appli
64	31	73.8	13	3	US-08-630-916A-87	Sequence 87, Appl
65	31	73.8	13	4	US-08-630-915A-143	Sequence 143, App
66	31	73.8	15	3	US-08-602-999A-301	Sequence 301, App
67	31	73.8	15	4	US-09-500-124-301	Sequence 301, App
68	31	73.8	16	3	US-08-602-999A-344	Sequence 344, App

69	31	73.8	16	4	US-09-500-124-344	Sequence 344, App
70	31	73.8	17	3	US-08-630-916A-10	Sequence 10, Appl
71	30	71.4	9	5	PCT-US94-01840-12	Sequence 12, Appl
72	30	71.4	10	3	US-08-348-518C-26	Sequence 26, Appl
73	30	71.4	10	3	US-08-476-509B-26	Sequence 26, Appl
74	30	71.4	12	3	US-08-602-999A-266	Sequence 266, App
75	30	71.4	12	4	US-09-500-124-266	Sequence 266, App
76	30	71.4	12	4	US-09-428-082B-312	Sequence 312, App
77	30	71.4	15	3	US-08-602-999A-373	Sequence 373, App
78	30	71.4	15	3	US-08-602-999A-382	Sequence 382, App
79	30	71.4	15	3	US-08-602-999A-415	Sequence 415, App
80	30	71.4	15	3	US-08-602-999A-430	Sequence 430, App
81	30	71.4	15	3	US-08-602-999A-431	Sequence 431, App
82	30	71.4	15	4	US-09-500-124-373	Sequence 373, App
83	30	71.4	15	4	US-09-500-124-382	Sequence 382, App
84	30	71.4	15	4	US-09-500-124-415	Sequence 415, App
85	30	71.4	15	4	US-09-500-124-430	Sequence 430, App
86	30	71.4	15	4	US-09-500-124-431	Sequence 431, App
87	30	71.4	16	3	US-08-602-999A-174	Sequence 174, App
88	30	71.4	16	3	US-08-602-999A-199	Sequence 199, App
89	30	71.4	16	4	US-09-500-124-174	Sequence 174, App
90	30	71.4	16	4	US-09-500-124-199	Sequence 199, App
91	30	71.4	17	3	US-08-602-999A-413	Sequence 413, App
92	30	71.4	17	4	US-09-500-124-413	Sequence 413, App
93	29	69.0	8	3	US-08-246-441-8	Sequence 8, Appli
94	29	69.0	8	4	US-09-393-585-8	Sequence 8, Appli
95	29	69.0	10	1	US-08-230-047-11	Sequence 11, Appl
96	29	69.0	10	3	US-08-602-999A-5	Sequence 5, Appli
97	29	69.0	10	4	US-08-278-865-5	Sequence 5, Appli
98	29	69.0	10	4	US-09-500-124-5	Sequence 5, Appli
99	29	69.0	11	1	US-08-336-343A-26	Sequence 26, Appl
100	29	69.0	11	3	US-08-602-999A-261	Sequence 261, App

# ALIGNMENTS

## RESULT 1

US-09-641-803-1

; Sequence 1, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-1

Query Match 100.0%; Score 42; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
| | | | | | |  
Db 1 MQPPPLP 7

RESULT 2

US-08-602-999A-278

; Sequence 278, Application US/08602999A

; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A

; FILING DATE: 16-FEB-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 278:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-278

Query Match 78.6%; Score 33; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:|||||  
Db 1 KPPPLP 6

RESULT 3

US-09-500-124-278

; Sequence 278, Application US/09500124  
; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 278:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-278

Query Match 78.6%; Score 33; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
:|||||  
Db 1 KPPPLP 6

RESULT 4

US-08-230-047-40

; Sequence 40, Application US/08230047  
; Patent No. 5541109

; GENERAL INFORMATION:

; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-230-047-40

Query Match 76.2%; Score 32; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 1 PPPLP 5

RESULT 5

PCT-US94-01840-11

; Sequence 11, Application PC/TUS9401840  
; GENERAL INFORMATION:  
; APPLICANT: Christopher E. Rudd  
; APPLICANT: Prasad Kanteti  
; APPLICANT: Lewis Cantley  
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF  
; TITLE OF INVENTION: LIPID KINASES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01840  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/023,915  
; FILING DATE: February 26, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janis K. Fraser  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00530/063001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: Linear  
PCT-US94-01840-11

Query Match 76.2%; Score 32; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||

Db 1 PPPLP 5

RESULT 6

US-09-641-640-8

; Sequence 8, Application US/09641640

; Patent No. RE37952

; GENERAL INFORMATION:

; APPLICANT: SCHWEIGHOFFER, Fabien

; TOCQUE, Bruno

; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd. 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/641,640

; FILING DATE: 15-Aug-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/612,857

; FILING DATE: <Unknown>

; APPLICATION NUMBER: WO PCT/FR94/00542

; FILING DATE: 09-MAY-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith Ph.D., Julie K.

; REGISTRATION NUMBER: 38,619

; REFERENCE/DOCKET NUMBER: ST93044-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610)454-3839

; TELEFAX: (610)454-3808

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..8

; OTHER INFORMATION: /note= "3BP1 peptide"

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:



US-09-641-640-8

Query Match 76.2%; Score 32; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 1 PPPLP 5

RESULT 7

US-08-612-857-8

; Sequence 8, Application US/08612857  
; Patent No. 5831048  
; GENERAL INFORMATION:  
; APPLICANT: SCHWEIGHOFFER, Fabien  
; APPLICANT: TOCQUE, Bruno  
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Rd. 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,857  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93-10971  
; FILING DATE: 15-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR94/00542  
; FILING DATE: 09-MAY-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph.D., Julie K.  
; REGISTRATION NUMBER: 38,619  
; REFERENCE/DOCKET NUMBER: ST93044-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3839  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal

; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..8  
; OTHER INFORMATION: /note= "3BP1 peptide"  
US-08-612-857-8

Query Match 76.2%; Score 32; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 1 PPPLP 5

RESULT 8

US-08-230-047-12

; Sequence 12, Application US/08230047  
; Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-12

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 5 PPPLP 9

RESULT 9

US-08-230-047-14

; Sequence 14, Application US/08230047  
; Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Searfoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-230-047-14

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||

Db 6 PPPLP 10

RESULT 10

US-08-212-190A-8

; Sequence 8, Application US/08212190A  
; Patent No. 5652223  
; GENERAL INFORMATION:  
; APPLICANT: KOHN, Elise C.  
; APPLICANT: LIOTTA, Lance A.  
; APPLICANT: KIM, Young Sook  
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/212,190A  
; FILING DATE: 14-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 15280-204US  
; REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-212-190A-8

Query Match 76.2%; Score 32; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 5 PPPLP 9

RESULT 11

US-08-900-321-8  
; Sequence 8, Application US/08900321  
; Patent No. 5981712  
; GENERAL INFORMATION:  
; APPLICANT: Kohn, Elise C.  
; APPLICANT: Liotta, Lance A.  
; APPLICANT: Kim, Young S.  
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/900,321  
; FILING DATE: 25-JUL-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,190  
; FILING DATE: 14-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-204100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-900-321-8

Query Match 76.2%; Score 32; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 12  
US-08-899-595-8  
; Sequence 8, Application US/08899595

```

; Patent No. 6111072
; GENERAL INFORMATION:
;   APPLICANT: Narumiya, Shuh
;   APPLICANT: Takahashi, No. 6111072uaki
;   TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
;   TITLE OF INVENTION: ENCODING SAME
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/899,595
;     FILING DATE: 24-JUL-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 8-242701
;     FILING DATE: 26-AUG-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 9-90170
;     FILING DATE: 25-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Stephen A. Bent
;     REGISTRATION NUMBER: 29,768
;     REFERENCE/DOCKET NUMBER: 049441/0112
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)672-5300
;     TELEFAX: (202)672-5399
;     TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 10
;     OTHER INFORMATION: /product= "G/S/A/V"
US-08-899-595-8

```

```

Query Match          76.2%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
            |||||
Db          4 PPPLP 8

```

RESULT 13

PCT-US95-03610-8

```
; Sequence 8, Application PC/TUS9503610
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION:  DNA ENCODING CAI RESISTANCE PROTEINS AND
;   TITLE OF INVENTION:  USES THEREOF
;   NUMBER OF SEQUENCES:  10
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US95/03610
;     FILING DATE:  14-MAR-1995
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/212,190
;     FILING DATE:  14-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Weber, Kenneth A.
;     REGISTRATION NUMBER:  31,677
;     REFERENCE/DOCKET NUMBER:  15280-204000PC
;     REFERENCE/DOCKET NUMBER:  DHHS Ref. No. E-112-94/0
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 543-9600
;     TELEFAX:  (415) 543-5043
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US95-03610-8
```

```
Query Match          76.2%;  Score 32;  DB 5;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 38;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 PPPLP 7
             |||||
Db          5 PPPLP 9
```

RESULT 14

US-08-336-343A-25

```
; Sequence 25, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
;   APPLICANT:  Ullrich, Axel
;   APPLICANT:  Alves, Frauke
;   TITLE OF INVENTION:  CCK-2, A No. 5677144el Receptor Tyrosine Kinase
;   NUMBER OF SEQUENCES:  43
```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/336,343A
;   FILING DATE:  08-NOV-1994
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Coruzzi, Laura A.
;   REGISTRATION NUMBER:  30,742
;   REFERENCE/DOCKET NUMBER:  7683-065
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  25:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-08-336-343A-25

```

```

Query Match          76.2%;  Score 32;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 41;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          4 PPPLP 8

```

# RESULT 15

US-08-652-877-22

; Sequence 22, Application US/08652877

; Patent No. 6187548

## ; GENERAL INFORMATION:

```

;   APPLICANT:  Akerstrom, Goran
;   APPLICANT:  Juhlin, Claes
;   APPLICANT:  Rask, Lars
;   APPLICANT:  Crumley, Gregg R.
;   APPLICANT:  Morse, Clarence C.
;   APPLICANT:  Murray, Edward M.
;   APPLICANT:  Hjalms, Goran
;   TITLE OF INVENTION:  Human Calcium Sensor Protein, Fragments
;   TITLE OF INVENTION:  Thereof and DNA Encoding Same
;   NUMBER OF SEQUENCES:  106
;   CORRESPONDENCE ADDRESS:

```



```

; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-22

```

```

Query Match          76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 41;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          4 PPPLP 8

```

```

RESULT 16
US-08-652-877-32
; Sequence 32, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran

```

```

; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-652-877-32

```

```

Query Match          76.2%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 41;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

Qy 3 PPPLP 7

Db                   11111  
                    4 PPPLP 8

RESULT 17

US-08-476-515A-22

; Sequence 22, Application US/08476515A

; Patent No. 6239270

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Martin Savitzky

; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;

; STREET: 3C43,

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 7.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,515A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE94/00483

; FILING DATE: 24-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9301764-8

; FILING DATE: 24-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-476-515A-22

Query Match 76.2%; Score 32; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | |  
Db 4 PPPLP 8

RESULT 18

US-08-476-515A-32

; Sequence 32, Application US/08476515A

; Patent No. 6239270

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 84

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Martin Savitzky

; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;

; STREET: 3C43,

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Compaq PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 7.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,515A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/SE94/00483

; FILING DATE: 24-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: SE 9301764-8

; FILING DATE: 24-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin  
 ; REGISTRATION NUMBER: 29,699  
 ; REFERENCE/DOCKET NUMBER: A1355D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-454-3816  
 ; TELEFAX: 610-454-3808  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; FRAGMENT TYPE: internal  
 US-08-476-515A-32

Query Match 76.2%; Score 32; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 |||||  
 Db 4 PPPLP 8

RESULT 19

US-08-230-047-17

; Sequence 17, Application US/08230047  
 ; Patent No. 5541109  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Searfoss III, George H.  
 ; APPLICANT: Ivashchenko, Yuri D.  
 ; APPLICANT: Jaye, Michael C.  
 ; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
 ; TITLE OF INVENTION: PROTEIN  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 ; STREET: 500 Arcola Road, 3C43  
 ; CITY: Collegeville  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19426  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Macintosh  
 ; OPERATING SYSTEM: System 7.1  
 ; SOFTWARE: Word 5.0 (PatentIn)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/230,047  
 ; FILING DATE: 19-APR-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goodman, Rosanne  
 ; REGISTRATION NUMBER: 32,534  
 ; REFERENCE/DOCKET NUMBER: A1465-US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-17

Query Match 76.2%; Score 32; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 4 PPPLP 8

RESULT 20

US-08-602-999A-251

; Sequence 251, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 251:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-251

Query Match 76.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | |  
Db 6 PPPLP 10

RESULT 21

US-08-602-999A-267

; Sequence 267, Application US/08602999A  
; Patent No. 6184205

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 267:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-267

Query Match 76.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 6 PPPLP 10

RESULT 22

US-09-500-124-251

; Sequence 251, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:



; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 251:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-251

Query Match 76.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 6 PPPLP 10

RESULT 23

US-09-500-124-267

; Sequence 267, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 267:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-267

Query Match 76.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 6 PPPLP 10

RESULT 24

US-09-845-917A-13  
; Sequence 13, Application US/09845917A  
; Patent No. 6653529  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-845-917A-13

Query Match 76.2%; Score 32; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 5 PPPLP 9

RESULT 25

US-09-845-917A-14  
; Sequence 14, Application US/09845917A  
; Patent No. 6653529

```
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-14
```

```
Query Match          76.2%; Score 32; DB 4; Length 13;
Best Local Similarity 57.1%; Pred. No. 49;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 MQPPPLP 7
          : |||:|
Db      3 LSPPPIP 9
```

#### RESULT 26

```
US-09-845-917A-19
; Sequence 19, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-845-917A-19
```

```
Query Match          76.2%; Score 32; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 49;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 PPPLP 7
          |||||
Db      6 PPPLP 10
```

RESULT 27

US-09-845-917A-21

; Sequence 21, Application US/09845917A  
 ; Patent No. 6653529  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bogaert, Thierry  
 ; APPLICANT: Vandekerckhove, Joel  
 ; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
 ; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
 ; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
 ; FILE REFERENCE: P/14-1  
 ; CURRENT APPLICATION NUMBER: US/09/845,917A  
 ; CURRENT FILING DATE: 2001-04-30  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 21  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Caenorhabditis elegans  
 US-09-845-917A-21

Query Match 76.2%; Score 32; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPLP 7  
 | | | | |  
 Db 5 PPPLP 9

RESULT 28

US-08-185-432-12

; Sequence 12, Application US/08185432  
 ; Patent No. 5750652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, Spyridon  
 ; APPLICANT: Busseau, Isabelle  
 ; APPLICANT: Diederich, Robert J.  
 ; APPLICANT: Xu, Tian  
 ; APPLICANT: Matsuno, Kenji  
 ; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
 ; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-185-432-12

```

```

Query Match          76.2%; Score 32; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      4 PPPLP 8

```

#### RESULT 29

US-08-630-916A-63

```

; Sequence 63, Application US/08630916A
; Patent No. 6011137

```

#### GENERAL INFORMATION:

```

; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME

```

```

; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711

```

#### COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

#### CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: MISROCK, S. LESLIE
;   REGISTRATION NUMBER: 18,872
;   REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 790-9090
;   TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 63:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 14 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-630-916A-63

```

```

Query Match          76.2%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 52;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      3 PPPLP 7
        |||||
Db      5 PPPLP 9

```

RESULT 30

US-08-630-915A-186

; Sequence 186, Application US/08630915A

; Patent No. 6309820

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. 6309820h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: McCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; TITLE OF INVENTION: USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

```

;     REGISTRATION NUMBER:  18,872
;     REFERENCE/DOCKET NUMBER:  1101-174
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 790-9090
;     TELEFAX:  (212) 869-8864/9741
;     TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  186:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH:  14 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
US-08-630-915A-186

```

```

Query Match          76.2%;  Score 32;  DB 4;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 52;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          5 PPPLP 9

```

RESULT 31

US-08-185-432-10

```

; Sequence 10, Application US/08185432
; Patent No. 5750652

```

; GENERAL INFORMATION:

```

; APPLICANT:  Artavanis-Tsakonas, Spyridon
; APPLICANT:  Busseau, Isabelle
; APPLICANT:  Diederich, Robert J.
; APPLICANT:  Xu, Tian
; APPLICANT:  Matsuno, Kenji
; TITLE OF INVENTION:  DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION:  ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES:  23
; CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  PENNIE & EDMONDS
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  U.S.A.
;     ZIP:  10036-2711

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER:  US/08/185,432
; FILING DATE:  21-JAN-1994
; CLASSIFICATION:  530

```

; ATTORNEY/AGENT INFORMATION:

```

; NAME:  Misrock, S. Leslie
; REGISTRATION NUMBER:  18,872
; REFERENCE/DOCKET NUMBER:  7326-006

```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-185-432-10

Query Match 76.2%; Score 32; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 32

US-08-769-745-31

; Sequence 31, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-08-769-745-31

Query Match 76.2%; Score 32; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 4 PPPLP 8

RESULT 33

US-08-602-999A-356

; Sequence 356, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.



```

; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-356

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
            |||||
Db          7 PPPLP 11

```

```

RESULT 34
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.

```

```

; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      3 PPPLP 7
        |||||
Db      7 PPPLP 11

```

```

RESULT 35
US-08-602-999A-404
; Sequence 404, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

```

```

; APPLICANT:  QUILLIAM, Lawrence A.
; APPLICANT:  DER, Channing J.
; APPLICANT:  FOWLKES, Dana M.
; APPLICANT:  RIDER, James E.
; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Pennie & Edmonds
; STREET:  1155 Avenue of the Americas
; CITY:  New York
; STATE:  New York
; COUNTRY:  U.S.A.
; ZIP:  10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/602,999A
; FILING DATE:  16-FEB-1996
; CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
; NAME:  Misrock, S. Leslie
; REGISTRATION NUMBER:  18,872
; REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (212) 790-9090
; TELEFAX:  (212) 869-9741/8864
; TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  404:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  15 amino acids
; TYPE:  amino acid
; TOPOLOGY:  unknown
; MOLECULE TYPE:  peptide
US-08-602-999A-404

```

```

Query Match          76.2%;  Score 32;  DB 3;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 56;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          4 PPPLP 8

```

#### RESULT 36

```

US-08-602-999A-414
; Sequence 414, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT:  SPARKS, Andrew B.
; APPLICANT:  KAY, Brian K.
; APPLICANT:  THORN, Judith M.
; APPLICANT:  QUILLIAM, Lawrence A.

```

```

; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-414

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          4 PPPLP 8

```

#### RESULT 37

```

US-08-602-999A-435
; Sequence 435, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.

```

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-435

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          4 PPPLP 8

```

```

RESULT 38
US-08-602-999A-436
; Sequence 436, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

```

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 436:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-436

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 57.1%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy          1 MQPPPLP 7
              : |||:|
Db          2 LSPPPIP 8

```

# RESULT 39

```

US-08-602-999A-441
; Sequence 441, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.

```

```

; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Pennie & Edmonds
; STREET:  1155 Avenue of the Americas
; CITY:  New York
; STATE:  New York
; COUNTRY:  U.S.A.
; ZIP:  10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/602,999A
; FILING DATE:  16-FEB-1996
; CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
; NAME:  Misrock, S. Leslie
; REGISTRATION NUMBER:  18,872
; REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (212) 790-9090
; TELEFAX:  (212) 869-9741/8864
; TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  441:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  15 amino acids
; TYPE:  amino acid
; TOPOLOGY:  unknown
; MOLECULE TYPE:  peptide
US-08-602-999A-441

```

```

Query Match          76.2%;  Score 32;  DB 3;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 56;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          5 PPPLP 9

```

#### RESULT 40

```

US-08-602-999A-452
; Sequence 452, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT:  SPARKS, Andrew B.
; APPLICANT:  KAY, Brian K.
; APPLICANT:  THORN, Judith M.
; APPLICANT:  QUILLIAM, Lawrence A.
; APPLICANT:  DER, Channing J.
; APPLICANT:  FOWLKES, Dana M.
; APPLICANT:  RIDER, James E.
; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF

```

```

; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-452

```

```

Query Match          76.2%; Score 32; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
             -|||||
Db          7 PPPLP 11

```

#### RESULT 41

US-09-500-124-356

; Sequence 356, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME



```

;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Pennie & Edmonds
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  U.S.A.
;     ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/500,124
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/602,999
;     FILING DATE:  16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Misrock, S. Leslie
;     REGISTRATION NUMBER:  18,872
;     REFERENCE/DOCKET NUMBER:  1101-202
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 790-9090
;     TELEFAX:  (212) 869-9741/8864
;     TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  356:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
US-09-500-124-356

```

```

Query Match          76.2%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 56;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          7 PPPLP 11

```

```

RESULT 42
US-09-500-124-385
; Sequence 385, Application US/09500124
; Patent No. 6432920
;   GENERAL INFORMATION:
;     APPLICANT:  SPARKS, Andrew B.
;     APPLICANT:  KAY, Brian K.
;     APPLICANT:  THORN, Judith M.
;     APPLICANT:  QUILLIAM, Lawrence A.
;     APPLICANT:  DER, Channing J.
;     APPLICANT:  FOWLKES, Dana M.
;     APPLICANT:  RIDER, James E.

```

```

; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/500,124
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/602,999
;   FILING DATE:  16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  385:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  15 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-09-500-124-385

```

```

Query Match          76.2%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 56;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          7 PPPLP 11

```

```

RESULT 43
US-09-500-124-404
; Sequence 404, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.

```

```

; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-404

```

```

Query Match          76.2%; Score 32; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
            |||||
Db          4 PPPLP 8

```

```

RESULT 44
US-09-500-124-414
; Sequence 414, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

```

```

; APPLICANT:  QUILLIAM, Lawrence A.
; APPLICANT:  DER, Channing J.
; APPLICANT:  FOWLKES, Dana M.
; APPLICANT:  RIDER, James E.
; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Pennie & Edmonds
; STREET:  1155 Avenue of the Americas
; CITY:  New York
; STATE:  New York
; COUNTRY:  U.S.A.
; ZIP:  10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  08/602,999
; FILING DATE:  16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME:  Misrock, S. Leslie
; REGISTRATION NUMBER:  18,872
; REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (212) 790-9090
; TELEFAX:  (212) 869-9741/8864
; TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  414:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  15 amino acids
; TYPE:  amino acid
; TOPOLOGY:  unknown
; MOLECULE TYPE:  peptide
US-09-500-124-414

```

```

Query Match          76.2%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 56;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          3 PPPLP 7
            |||||
Db          4 PPPLP 8

```

```

RESULT 45
US-09-500-124-435
; Sequence 435, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT:  SPARKS, Andrew B.

```

; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 435:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-09-500-124-435

Query Match 76.2%; Score 32; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 4 PPPLP 8

RESULT 46  
 US-09-500-124-436  
 ; Sequence 436, Application US/09500124  
 ; Patent No. 6432920

```

; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Pennie & Edmonds
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  U.S.A.
;     ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/500,124
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/602,999
;     FILING DATE:  16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Misrock, S. Leslie
;     REGISTRATION NUMBER:  18,872
;     REFERENCE/DOCKET NUMBER:  1101-202
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 790-9090
;     TELEFAX:  (212) 869-9741/8864
;     TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  436:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
US-09-500-124-436

```

```

Query Match          76.2%;  Score 32;  DB 4;  Length 15;
Best Local Similarity 57.1%;  Pred. No. 56;
Matches      4;  Conservative  2;  Mismatches  1;  Indels    0;  Gaps    0;

```

```

Qy          1 MQPPPLP 7
              : |||:|
Db          2 LSPPPIP 8

```

```

RESULT 47
US-09-500-124-441

```

```

; Sequence 441, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
;   APPLICANT: SPARKS, Andrew B.
;   APPLICANT: KAY, Brian K.
;   APPLICANT: THORN, Judith M.
;   APPLICANT: QUILLIAM, Lawrence A.
;   APPLICANT: DER, Channing J.
;   APPLICANT: FOWLKES, Dana M.
;   APPLICANT: RIDER, James E.
;   TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION: ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES: 467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/500,124
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/602,999
;     FILING DATE: 16-FEB-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Misrock, S. Leslie
;     REGISTRATION NUMBER: 18,872
;     REFERENCE/DOCKET NUMBER: 1101-202
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 790-9090
;     TELEFAX: (212) 869-9741/8864
;     TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 441:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       TOPOLOGY: unknown
;     MOLECULE TYPE: peptide
US-09-500-124-441

```

```

Query Match          76.2%; Score 32; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          5 PPPLP 9

```

RESULT 48  
 US-09-500-124-452  
 ; Sequence 452, Application US/09500124  
 ; Patent No. 6432920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME  
 ; NUMBER OF SEQUENCES: 467  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/500,124  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 452:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-09-500-124-452

Query Match 76.2%; Score 32; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 | | | |  
 Db 7 PPPLP 11



RESULT 49

US-08-185-432-9

```
; Sequence 9, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
;   APPLICANT: Artavanis-Tsakonas, Spyridon
;   APPLICANT: Busseau, Isabelle
;   APPLICANT: Diederich, Robert J.
;   APPLICANT: Xu, Tian
;   APPLICANT: Matsuno, Kenji
;   TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
;   TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
;   NUMBER OF SEQUENCES: 23
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: PENNIE & EDMONDS
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/185,432
;     FILING DATE: 21-JAN-1994
;     CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Misrock, S. Leslie
;     REGISTRATION NUMBER: 18,872
;     REFERENCE/DOCKET NUMBER: 7326-006
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 790-9090
;     TELEFAX: (212) 869-8864/9741
;     TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 16 amino acids
;       TYPE: amino acid
;       TOPOLOGY: unknown
;     MOLECULE TYPE: peptide
```

US-08-185-432-9

```
Query Match          76.2%; Score 32; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 59;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          3 PPPLP 7
             |||||
Db          6 PPPLP 10
```

RESULT 50

US-08-185-432-14  
 ; Sequence 14, Application US/08185432  
 ; Patent No. 5750652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, Spyridon  
 ; APPLICANT: Busseau, Isabelle  
 ; APPLICANT: Diederich, Robert J.  
 ; APPLICANT: Xu, Tian  
 ; APPLICANT: Matsuno, Kenji  
 ; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
 ; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/185,432  
 ; FILING DATE: 21-JAN-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 7326-006  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864/9741  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 16 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-08-185-432-14

Query Match 76.2%; Score 32; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 6 PPPLP 10

Search completed: July 4, 2004, 04:48:43  
 Job time : 5.38806 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 5.3806 Seconds  
 (without alignments)  
 125.142 Million cell updates/sec

Title: US-09-641-802-1  
 Perfect score: 42  
 Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7  
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	32	76.2	18	2	PC2280	prolylendopeptidas
2	27	64.3	15	2	B39109	hypothetical 1.5K
3	26	61.9	7	2	S71299	ICL2 protein - Par
4	25	59.5	10	2	A36454	trypsin-modulating
5	25	59.5	13	2	A60856	inhibin alpha chai
6	25	59.5	13	2	S09716	2S albumin large c
7	25	59.5	14	2	S11129	phosphoprotein, bo
8	25	59.5	15	2	PT0037	light harvesting c
9	25	59.5	16	2	E58503	superoxide dismuta
10	25	59.5	17	2	S57991	hydroxyproline-ric
11	24	57.1	11	2	I33098	173K exoantigen -
12	23	54.8	11	1	XAVIBH	bradykinin-potenti
13	23	54.8	13	2	S21152	tryptophyllin-rela

14	23	54.8	13	2	A05174	tryptophyllin-13 -
15	23	54.8	17	2	S59481	hydroxyproline-ric
16	22	52.4	12	2	PA0098	ribosomal protein
17	22	52.4	15	2	B35389	urease (EC 3.5.1.5
18	22	52.4	17	2	A49237	45/47K antigen - M
19	22	52.4	18	2	I52614	u-plasminogen acti
20	22	52.4	18	2	A54195	Na+/K+-exchanging
21	21	50.0	11	2	D45900	complement C3b rec
22	21	50.0	12	2	PN0663	dystrophin-associa
23	21	50.0	12	2	B39690	neural cell adhesi
24	21	50.0	13	2	D39690	neural cell adhesi
25	21	50.0	14	2	S12904	protein kinase (EC
26	21	50.0	15	2	PQ0545	capsid protein VP1
27	21	50.0	16	2	JH0517	insulin-like growt
28	20	47.6	10	2	H28027	protein P11 - curl
29	20	47.6	13	2	A40207	cell surface glyco
30	20	47.6	15	2	S67918	serine proteinase
31	20	47.6	15	2	PA0002	photosystem II oxy
32	19.5	46.4	14	2	H64008	hypothetical prote
33	19	45.2	7	2	PT0283	Ig heavy chain CRD
34	19	45.2	10	2	B59272	peptide-N4-(N-acet
35	19	45.2	11	1	XASNBA	bradykinin-potenti
36	19	45.2	11	2	YHRT	morphogenetic neur
37	19	45.2	11	2	YHHU	morphogenetic neur
38	19	45.2	11	2	YHBO	morphogenetic neur
39	19	45.2	11	2	YHXAE	morphogenetic neur
40	19	45.2	11	2	YHJFHY	morphogenetic neur
41	19	45.2	11	2	C37196	bradykinin-potenti
42	19	45.2	11	2	D37196	bradykinin-potenti
43	19	45.2	13	2	G61458	Ig lambda chain V-
44	19	45.2	13	2	A86126	hypothetical prote
45	19	45.2	15	2	PA0088	protein QF200051 -
46	19	45.2	15	2	A60221	apolipoprotein A-I
47	19	45.2	16	2	C49048	T-cell receptor be
48	19	45.2	17	2	I49593	cystic fibrosis tr
49	19	45.2	17	2	I84733	gene CFTR protein
50	19	45.2	17	2	S05033	photosystem II pro
51	19	45.2	17	2	PT0235	Ig heavy chain CRD
52	19	45.2	17	2	S10786	enamelin, 26K - bo
53	19	45.2	17	2	B25348	glycogen(starch) s
54	18	42.9	8	2	B39745	endoglycosylcerami
55	18	42.9	8	2	S10783	enamelin f - bovin
56	18	42.9	9	2	B41983	orf downstream to b
57	18	42.9	10	2	PC2171	triacylglycerol li
58	18	42.9	10	2	C39745	sphingomyelinase -
59	18	42.9	11	2	S07203	uperolein - frog (
60	18	42.9	13	2	I84603	deoxynucleotidyltr
61	18	42.9	14	2	B60683	malate dehydrogena
62	18	42.9	15	2	A35232	gentisate 1,2-diox
63	18	42.9	15	2	S27248	pseudogermin - whe
64	18	42.9	15	2	PA0060	protein QF200037 -
65	18	42.9	15	2	B61457	alpha-glucosidase
66	18	42.9	16	2	I57530	gene c-fms protein
67	18	42.9	16	2	PH1302	Ig heavy chain DJ
68	18	42.9	16	2	S57517	T cell receptor be
69	18	42.9	16	2	JT0609	leukocyte chemoatt
70	18	42.9	17	2	S33609	extensin - maize (

71	18	42.9	17	2	A42920	fatty acid ethyl e
72	18	42.9	18	2	S04229	N4-(beta-N-acetylgl
73	17	40.5	9	2	S26508	collagen alpha 2(V
74	17	40.5	10	2	H37196	bradykinin-potenti
75	17	40.5	11	2	D60409	kassinin-like pept
76	17	40.5	11	2	F60409	substance P-like p
77	17	40.5	11	2	E60409	substance P-like p
78	17	40.5	11	2	B60409	kassinin-like pept
79	17	40.5	11	2	C60409	kassinin-like pept
80	17	40.5	11	2	D56979	collagen alpha 1(I
81	17	40.5	12	2	S07436	tachykinin - Afric
82	17	40.5	12	2	S70337	napin small chain
83	17	40.5	15	2	A60929	dichloromethane de
84	17	40.5	15	2	B60929	dichloromethane de
85	17	40.5	15	2	PA0014	seed storage prote
86	17	40.5	15	2	PN0173	seed storage prote
87	17	40.5	15	2	PA0071	superoxide dismuta
88	17	40.5	18	2	C56211	progesterone recep
89	17	40.5	18	2	A40760	basic fibroblast g
90	16	38.1	8	2	PT0559	T-cell receptor be
91	16	38.1	10	1	XAVI6B	angiotensin-conver
92	16	38.1	10	2	B37196	bradykinin-potenti
93	16	38.1	11	2	C61497	seed protein ws-18
94	16	38.1	11	2	PH1583	Ig H chain V-D-J r
95	16	38.1	11	2	PN0042	stathmin - mouse (
96	16	38.1	11	2	I52304	gene rSSTR4 protei
97	16	38.1	12	2	E45691	probable minor cap
98	16	38.1	12	2	JU0356	cycloleonorinin -
99	16	38.1	12	2	PQ0786	NADH2 dehydrogenas
100	16	38.1	14	2	A61002	photosystem II oxy

#### ALIGNMENTS

##### RESULT 1

PC2280

prolylendopeptidase-inhibiting peptide - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997

C;Accession: PC2280

R;Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.

Biochem. Biophys. Res. Commun. 202, 809-815, 1994

A;Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.

A;Reference number: PC2280; MUID:94324971; PMID:8048952

A;Accession: PC2280

A;Molecule type: protein

A;Residues: 1-18 <OHM>

A;Experimental source: brain

C;Superfamily: cytoskeletal keratin

Query Match 76.2%; Score 32; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|||||

## RESULT 2

B39109

hypothetical 1.5K protein - hepatitis C virus

N;Alternate names: hypothetical protein 2

C;Species: hepatitis C virus

C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999

C;Accession: B39109; JQ1585

R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.;  
Tekamp-Olson, P.; Kuo, G.; Choo, Q.L.; Houghton, M.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A;Title: Characterization of the terminal regions of hepatitis C viral RNA:  
identification of conserved sequences in the 5' untranslated region and poly(A)  
tails at the 3' end.

A;Reference number: A39109; MUID:91156678; PMID:1705704

A;Accession: B39109

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-15 &lt;HAN&gt;

A;Cross-references: GB:M58406

R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992

A;Title: Cloning and sequencing of the structural region and expression of  
putative core gene of hepatitis C virus from a British case of chronic sporadic  
hepatitis.

A;Reference number: JQ1584; MUID:92300349; PMID:1318944

A;Accession: JQ1585

A;Molecule type: genomic RNA

A;Residues: 1-15 &lt;KUM&gt;

A;Experimental source: strain U.K.

Query Match 64.3%; Score 27; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MQP--PPLP 7

:|| |||

Db 4 VQPPGPPLP 12

## RESULT 3

S71299

ICL2 protein - Paramecium tetraurelia (fragment)

C;Species: Paramecium tetraurelia

C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999

C;Accession: S71299

R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A;Title: Characterization of centrin genes in Paramecium.

A;Reference number: S71298; MUID:96248429; PMID:8665928

A;Accession: S71299

A;Molecule type: protein

A;Residues: 1-7 &lt;MAD&gt;

A;Experimental source: strain d4-2

C;Genetics:

A;Genetic code: SGC5

Query Match 61.9%; Score 26; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPP 5  
    ||||  
Db 2 QPPP 5

RESULT 4

A36454

trypsin-modulating oostatic factor - yellow fever mosquito

C;Species: *Aedes aegypti* (yellow fever mosquito)

C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-May-1996

C;Accession: A36454; A61630

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

FASEB J. 4, 3015-3020, 1990

A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme biosynthesis in the midgut.

A;Reference number: A36454; MUID:90367888; PMID:2394318

A;Accession: A36454

A;Molecule type: protein

A;Residues: 1-10 <BOR>

R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.

Insect Biochem. Mol. Biol. 23, 703-712, 1993

A;Title: Mass spectrometry and characterization of *Aedes aegypti* trypsin modulating oostatic factor (TMOF) and its analogs.

A;Reference number: A61630; MUID:93357794; PMID:8353526

A;Accession: A61630

A;Molecule type: protein

A;Residues: 1-10 <BO2>

A;Note: none of the amino acids is modified

C;Function:

A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut epithelial cells

C;Keywords: hormone

Query Match 59.5%; Score 25; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
    ||| |  
Db 5 PPPPP 9

RESULT 5

A60856

inhibin alpha chain - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: A60856

R;Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.;

Wettenhall, R.E.H.; Findlay, J.K.; Burger, H.G.; de Kretser, D.M.

J. Endocrinol. 113, 213-221, 1987

A;Title: Isolation of inhibin from ovine follicular fluid.  
A;Reference number: A60856; MUID:87224684; PMID:3585232  
A;Accession: A60856  
A;Molecule type: protein  
A;Residues: 1-13 <LEV>  
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.  
C;Superfamily: inhibin  
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 59.5%; Score 25; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
| | | |  
Db 3 PPLP 6

#### RESULT 6

S09716

2S albumin large chain (1 and 2) nII - rape (fragments)

N;Alternate names: 2S albumin large chain nIII

C;Species: Brassica napus (rape)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Aug-1998

C;Accession: S09716; S09718; S09717

R;Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.

FEBS Lett. 263, 209-212, 1990

A;Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins.

A;Reference number: S09720; MUID:90242974; PMID:2185951

A;Accession: S09716

A;Molecule type: protein

A;Residues: 1-9;10-13 <MON>

A;Experimental source: seed

A;Note: 3-Ser was also found

A;Accession: S09718

A;Molecule type: protein

A;Residues: 1-9;10-13 <MO2>

A;Experimental source: seed

A;Accession: S09717

A;Molecule type: protein

A;Residues: 1-9;10-13 <MO3>

A;Experimental source: seed

Query Match 59.5%; Score 25; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
: | | | |  
Db 7 RPPPGP 12

#### RESULT 7

S11129

phosphoprotein, bone - chicken (fragment)

C;Species: Gallus gallus (chicken)



C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 25-Oct-1996  
C;Accession: S11129  
R;Mikuni-Takagaki, Y.; Glimcher, M.J.  
Biochem. J. 268, 585-591, 1990  
A;Title: Post-translational processing of chicken bone phosphoproteins.  
Identification of the bone phosphoproteins of embryonic tibia.  
A;Reference number: S11127; MUID:90303246; PMID:2363696  
A;Accession: S11129  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <MIK>  
C;Keywords: phosphoprotein

Query Match 59.5%; Score 25; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6  
    ||||  
Db 5 PPPL 8

#### RESULT 8

PT0037

light harvesting complex chain III/b, photosystem I - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993

C;Accession: PT0037; PS0205

R;Uchiyama, Y.; Tsugita, A.

submitted to JIPID, June 1991

A;Reference number: PS0189

A;Accession: PT0037

A;Molecule type: protein

A;Residues: 1-15 <UCH>

Query Match 59.5%; Score 25; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
    ||| |  
Db 8 PPPPP 12

#### RESULT 9

E58503

superoxide dismutase (EC 1.15.1.1) - unidentified bacterium (fragment)

N;Alternate names: 21.3K bladder and kidney stone protein

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 05-Mar-1999

C;Accession: E58503

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: E58503

A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-16 <BIN>  
A;Experimental source: human bladder and kidney stones  
C;Function:  
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen and hydrogen peroxide  
C;Keywords: metalloprotein; oxidoreductase

Query Match 59.5%; Score 25; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
||||  
Db 6 PPLP 9

RESULT 10

S57991

hydroxyproline-rich protein - *Sesbania rostrata* (fragment)

C;Species: *Sesbania rostrata*

C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 11-Jan-2000

C;Accession: S57991

R;Goormachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.; de Bruijn, F.

submitted to the EMBL Data Library, March 1995

A;Description: Use of differential display to identify novel *Sesbania rostrata* genes enhanced by *Azorhizobium caulinodans* infection.

A;Reference number: S57991

A;Accession: S57991

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-17 <GOO>

A;Cross-references: EMBL:Z48673; NID:g899484; PID:g899485

C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 59.5%; Score 25; DB 2; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
||| |  
Db 10 PPPPP 14

RESULT 11

I33098

173K exoantigen - malaria parasite (*Plasmodium falciparum*) (fragments)

C;Species: *Plasmodium falciparum*

C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C;Accession: I33098

R;Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: I33098

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIC>

Query Match 57.1%; Score 24; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|| ||  
Db 3 PPELP 7

#### RESULT 12

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 4.2e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
||:|  
Db 7 PPIP 10

#### RESULT 13

S21152

tryptophyllin-related peptide - two-colored leaf frog

C;Species: Phyllomedusa bicolor (two-colored leaf frog)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S21152

R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.; Barra, D.

FEBS Lett. 302, 151-154, 1992

A;Title: Identification and characterization of two dermorphins from skin extracts of the Amazonian frog Phyllomedusa bicolor.

A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152

A;Molecule type: protein

A;Residues: 1-13 <MIG>  
A;Experimental source: skin  
C;Superfamily: unassigned animal peptides

Query Match 54.8%; Score 23; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 4.9e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6  
|||:  
Db 7 PPPI 10

#### RESULT 14

A05174

tryptophyllin-13 - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Aug-2000

C;Accession: A05174

R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.

Int. J. Pept. Protein Res. 27, 175-182, 1986

A;Reference number: A05174

A;Accession: A05174

A;Molecule type: protein

A;Residues: 1-13 <MON>

C;Superfamily: unassigned animal peptides

C;Keywords: pyroglutamic acid; skin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 4.9e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6  
|||:  
Db 7 PPPI 10

#### RESULT 15

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)

C;Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998

C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.

Plant Mol. Biol. 28, 1075-1087, 1995

A;Title: Specificity in the immobilisation of cell wall proteins in response to different elicitor molecules in suspension-cultured cells of French bean (Phaseolus vulgaris L.).

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 54.8%; Score 23; DB 2; Length 17;

Best Local Similarity 57.1%; Pred. No. 6.5e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
| ||:  
Db 2 MYLPPVP 8

RESULT 16

PA0098

ribosomal protein S3 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0098

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* proteins.

A;Reference number: PA0051

A;Accession: PA0098

A;Molecule type: protein

A;Residues: 1-12 <CHO>

Query Match 52.4%; Score 22; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 6.4e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
||:  
Db 4 PPVP 7

RESULT 17

B35389

urease (EC 3.5.1.5) 15K chain - *Morganella morganii* (fragment)

C;Species: *Morganella morganii*

C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993

C;Accession: B35389

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
J. Bacteriol. 172, 3073-3080, 1990

A;Title: *Morganella morganii* urease: purification, characterization, and isolation of gene sequences.

A;Reference number: A35389; MUID:90264298; PMID:2345135

A;Accession: B35389

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <HUA>

C;Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPPL 6  
|| ||  
Db 5 QPTPL 9

RESULT 18

A49237

45/47K antigen - Mycobacterium bovis (fragment)

C;Species: Mycobacterium bovis

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995

C;Accession: A49237

R;Romain, F.; Laqueyrie, A.; Militzer, P.; Pescher, P.; Chavarot, P.;

Lagranderie, M.; Auregan, G.; Gheorghiu, M.; Marchal, G.

Infect. Immun. 61, 742-750, 1993

A;Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, an immunodominant target for antibody response after immunization with living bacteria.

A;Reference number: A49237; MUID:93138802; PMID:8423100

A;Contents: BCG

A;Accession: A49237

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <ROM>

A;Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 52.4%; Score 22; DB 2; Length 17;

Best Local Similarity 75.0%; Pred. No. 9.1e+02;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7

||:

Db 6 PPVP 9

RESULT 19

I52614

u-plasminogen activator receptor precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000

C;Accession: I52614

R;Soravia, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

Blood 86, 624-635, 1995

A;Title: A conserved TATA-less proximal promoter drives basal transcription from the urokinase-type plasminogen activator receptor gene.

A;Reference number: I52614; MUID:95329719; PMID:7605992

A;Accession: I52614

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-18 <RES>

A;Cross-references: GB:S78532; NID:g999307; PIDN:AAD14289.1; PID:g4261989

C;Genetics:

A;Gene: uPAR

C;Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 52.4%; Score 22; DB 2; Length 18;

Best Local Similarity 80.0%; Pred. No. 9.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7

|| ||

## RESULT 20

A54195

Na<sup>+</sup>/K<sup>+</sup>-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002

C;Accession: A54195

R;Esmann, M.; Karlish, S.J.; Sottrup-Jensen, L.; Marsh, D.

Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase from shark rectal glands.

A;Reference number: A54195; MUID:94297020; PMID:8025109

A;Accession: A54195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 &lt;ESM&gt;

A;Experimental source: rectal gland

A;Note: sequence extracted from NCBI backbone (NCBIP:149363)

C;Keywords: hydrolase

Query Match 52.4%; Score 22; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 9.7e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5  
: |||  
Db 6 LTPPP 10

## RESULT 21

D45900

complement C3b receptor type 2 - mouse (clone 12) (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: D45900

R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.

J. Immunol. 144, 3581-3591, 1990

A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1.

A;Reference number: A45900; MUID:90229754; PMID:2139460

A;Accession: D45900

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-11 &lt;KUR&gt;

Query Match 50.0%; Score 21; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 9 PPP 11

# RESULT 22

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C;Accession: PN0663

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in Duchenne muscular dystrophy muscle.

A;Reference number: PN0662; MUID:94156881; PMID:8113213

A;Accession: PN0663

A;Molecule type: protein

A;Residues: 1-12 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 50.0%; Score 21; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.1e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5

|||

Db 5 PPP 7

# RESULT 23

B39690

neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C;Accession: B39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expressed during rat heart development.

A;Reference number: A39690; MUID:91141516; PMID:1996115

A;Accession: B39690

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-12 <REY>

A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 21; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.1e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5

|||

Db 6 PPP 8

# RESULT 24

D39690



neural cell adhesion molecule, cardiac splice form +,-,-,+ - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C;Accession: D39690  
 R;Reyes, A.A.; Small, S.J.; Akeson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA are expressed during rat heart development.  
 A;Reference number: A39690; MUID:91141516; PMID:1996115  
 A;Accession: D39690  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-13 <REY>  
 A;Cross-references: GB:M63970  
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin homology  
 C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 21; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 6 PPP 8

#### RESULT 25

S12904  
 protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)  
 C;Species: Pisaster ochraceus  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
 C;Accession: S12904  
 R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.  
 FEBS Lett. 273, 223-226, 1990  
 A;Title: Identification of the sites in myelin basic protein that are phosphorylated by meiosis-activated protein kinase p44(mpk).  
 A;Reference number: S12904; MUID:91032186; PMID:1699809  
 A;Accession: S12904  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <SAN>  
 C;Keywords: phosphotransferase

Query Match 50.0%; Score 21; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 8 PPP 10

#### RESULT 26

PQ0545  
 capsid protein VP19C - human herpesvirus 1 (fragment)

C;Species: human herpesvirus 1  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
 C;Accession: PQ0545  
 R;Davison, M.D.; Rixon, F.J.; Davison, A.J.  
 J. Gen. Virol. 73, 2709-2713, 1992  
 A;Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes simplex virus type 1.  
 A;Reference number: PQ0544; MUID:93019027; PMID:1328483  
 A;Accession: PQ0545  
 A;Molecule type: protein  
 A;Residues: 1-15 <DAV>  
 A;Experimental source: strain 17  
 C;Genetics:  
 A;Gene: UL38  
 C;Keywords: capsid protein

Query Match 50.0%; Score 21; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MQPPPLP 7  
 | : | | |  
 Db 1 MKTNPLP 7

#### RESULT 27

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 03-Nov-2003

C;Accession: JH0517

R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.

Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991

A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth factor-binding proteins in porcine serum.

A;Reference number: JH0515; MUID:92109718; PMID:1722398

A;Accession: JH0517

A;Molecule type: protein

A;Residues: 1-16 <COL>

A;Experimental source: serum

C;Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat homology

Query Match 50.0%; Score 21; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 | | |  
 Db 7 PPP 9

#### RESULT 28

H28027

protein P11 - curled-leaved tobacco (fragment)

C;Species: Nicotiana glauca (curled-leaved tobacco)

C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C;Accession: H28027

R;Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A;Title: Alterations in the phenotype of plant cells studied by NH2-terminal  
amino acid-sequence analysis of proteins electroblotted from two-dimensional  
gel-separated total extracts.

A;Reference number: A94167

A;Accession: H28027

A;Molecule type: protein

A;Residues: 1-10 <BAU>

A;Note: 4-Val was also found

Query Match 47.6%; Score 20; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 7 PPXP 10

#### RESULT 29

A40207

cell surface glycoprotein gp150 - slime mold (*Dictyostelium discoideum*)  
(fragment)

C;Species: *Dictyostelium discoideum*

C;Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 31-Dec-1993

C;Accession: A40207

R;Gao, E.N.; Shier, P.; Siu, C.H.

J. Biol. Chem. 267, 9409-9415, 1992

A;Title: Purification and partial characterization of a cell adhesion molecule  
(gp150) involved in postaggregation stage cell-cell binding in *Dictyostelium*  
*discoideum*.

A;Reference number: A40207; MUID:92250549; PMID:1577768

A;Accession: A40207

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <GAO>

C;Keywords: glycoprotein

Query Match 47.6%; Score 20; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 3 PPTP 6

#### RESULT 30

S67918

serine proteinase lasD (EC 3.4.21.-), staphylolytic - *Pseudomonas aeruginosa*  
(fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997

C;Accession: S67918

R;Park, S.; Galloway, D.R.

Mol. Microbiol. 16, 263-270, 1995

A;Title: Purification and characterization of LasD: a second staphylolytic proteinase produced by *Pseudomonas aeruginosa*.

A;Reference number: S67918; MUID:96015439; PMID:7565088

A;Accession: S67918

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <PAR>

C;Genetics:

A;Gene: lasD

C;Keywords: hydrolase; serine proteinase

Query Match 47.6%; Score 20; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5  
|: ||  
Db 4 METPP 8

#### RESULT 31

PA0002

photosystem II oxygen-evolving complex protein 3 - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 18-Nov-1994 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C;Accession: PA0002

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of *Arabidopsis* proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0002

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: stem

C;Keywords: photosynthesis; photosystem II

Query Match 47.6%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 10 PPXP 13

#### RESULT 32

H64008

hypothetical protein HI0492 - *Haemophilus influenzae* (strain Rd KW20)

C;Species: *Haemophilus influenzae*

C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998

C;Accession: H64008

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.;

Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.;

McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;

Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64008

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <TIGR>

A;Cross-references: GB:U32731; GB:L42023; NID:g1573465; PID:g1573478;

TIGR:HI0492

Query Match 46.4%; Score 19.5; DB 2; Length 14;

Best Local Similarity 41.7%; Pred. No. 1.8e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

Qy 1 MQP-----PPLP 7

|:| |||

Db 1 MKPKYPKMPPKP 12

#### RESULT 33

PT0283

Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0283

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0283

A;Molecule type: DNA

A;Residues: 1-7 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 45.2%; Score 19; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

|||

Db 5 QPP 7

#### RESULT 34

B59272

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain - sweet almond (fragment)

N;Alternate names: peptide N-glycosidase

C;Species: *Prunus dulcis* var. *sativa* (sweet almond)  
 C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000  
 C;Accession: B59272  
 R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.  
 Eur. J. Biochem. 252, 118-123, 1998  
 A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminy1)asparagine  
 amidase A and its N-glycans.  
 A;Reference number: A59272; MUID:98181894; PMID:9523720  
 A;Accession: B59272  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <ALT>  
 C;Keywords: hydrolase

Query Match 45.2%; Score 19; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPPL 6  
 :| ||  
 Db 1 EPTPL 5

#### RESULT 35

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: *Agkistrodon blomhoffi* (mamushi)  
 C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995  
 C;Accession: A01254  
 R;Kato, H.; Suzuki, T.  
 Proc. Jpn. Acad. 46, 176-181, 1970  
 A;Reference number: A01254  
 A;Accession: A01254  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAT>  
 A;Note: the sequence of the natural peptide was confirmed by the synthesis and  
 analysis of a peptide having the identical structure and biological properties  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic  
 acid; venom  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
 || |  
 Db 4 PPRP 7

#### RESULT 36

YHRT

morphogenetic neuropeptide - rat

C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.  
 Nature 293, 579-580, 1981  
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator,  
 from coelenterates to humans.  
 A;Reference number: A93266; MUID:82035850; PMID:7290191  
 A;Accession: A01427  
 A;Molecule type: protein  
 A;Residues: 1-11 <BOD>  
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
 FEBS Lett. 131, 317-321, 1981  
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
 A;Reference number: A91296; MUID:82050803; PMID:7297679  
 A;Contents: annotation; synthesis  
 A;Note: the synthetic peptide was identical with the natural peptide in chemical  
 structure and biological activity  
 C;Comment: This peptide was first isolated from nerve cells of hydra and was  
 called head activator by the authors, because it induced head-specific growth  
 and differentiation in this animal. It has been found in mammalian intestine and  
 hypothalamus.  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide;  
 pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
 |||  
 Db 1 QPP 3

#### RESULT 37

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator,  
 from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical  
 structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was  
 called head activator because it induced head-specific growth and

differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

|||

Db 1 QPP 3

#### RESULT 38

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

|||

Db 1 QPP 3



# RESULT 39

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4

|||

Db 1 QPP 3

# RESULT 40

YHJFHY

morphogenetic neuropeptide - *Hydra attenuata*

N;Alternate names: head activator

C;Species: *Hydra attenuata*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
|||  
Db 1 QPP 3

#### RESULT 41

C37196

bradykinin-potentiating peptide 3 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: C37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: C37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 4 PPRP 7

#### RESULT 42

D37196

bradykinin-potentiating peptide 4 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: D37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from *Bothrops insularis* snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: D37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 45.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||

Db 4 PPRP 7

#### RESULT 43

G61458

Ig lambda chain V-II region (AZI) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996

C;Accession: G61458; PL0159

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein and characterization of the variability subgroup of their heavy and light chains.

A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Accession: G61458

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein.

C;Keywords: heterotetramer; immunoglobulin

Query Match 45.2%; Score 19; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
|||

Db 6 QPP 8

#### RESULT 44

A86126

hypothetical protein Z5883 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)

C;Species: *Escherichia coli*

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C;Accession: A86126

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.;

Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A86126

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-13 <STO>

A;Cross-references: GB:AE005174; NID:g12519285; PIDN:AAG59469.1; GSPDB:GN00145; UWGP:Z5883

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z5883

Query Match 45.2%; Score 19; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
||| |  
Db 1 MQPDKL 6

#### RESULT 45

PA0088

protein QF200051 - fungus (*Fusarium sporotrichioides*) (fragment)

C;Species: *Fusarium sporotrichioides*

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C;Accession: PA0088

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* proteins.

A;Reference number: PA0051

A;Accession: PA0088

A;Molecule type: protein

A;Residues: 1-15 <CHO>

Query Match 45.2%; Score 19; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
| | :|  
Db 1 QKPDIP 6

#### RESULT 46

A60221

apolipoprotein A-I - common carp (fragment)

C;Species: *Cyprinus carpio* (common carp)

C;Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993

C;Accession: A60221

R;Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.  
J. Neurochem. 55, 1237-1243, 1990

A;Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve regeneration.  
A;Reference number: A60221; MUID:90376100; PMID:2118944  
A;Accession: A60221  
A;Molecule type: protein  
A;Residues: 1-15 <HAR>  
A;Note: protein from plasma and from optic nerve yielded the same sequence  
C;Keywords: lipid binding; lipoprotein

Query Match 45.2%; Score 19; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
|||  
Db 2 QPP 4

RESULT 47

C49048

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C;Accession: C49048

R;Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2418, 1992

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile rheumatoid arthritis synovial T cells.

A;Reference number: A49048; MUID:92387250; PMID:1387614

A;Accession: C49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113265)

C;Keywords: T-cell receptor

Query Match 45.2%; Score 19; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5  
:| ||  
Db 7 LQGPP 11

RESULT 48

I49593

cystic fibrosis transmembrane conductance regulator - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999

C;Accession: I49593

R;Denamur, E.; Chehab, F.F.

Hum. Mol. Genet. 3, 1089-1094, 1994

A;Title: Analysis of the mouse and rat CFTR promoter regions.

A;Reference number: I49593; MUID:95072572; PMID:7526924  
A;Accession: I49593  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-17 <RES>  
A;Cross-references: GB:L04873; NID:g414726; PIDN:AAA73562.1; PID:g553892  
C;Genetics:  
A;Gene: CFTR  
C;Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette homology

Query Match 45.2%; Score 19; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
|| ||  
Db 1 MQKSPL 6

RESULT 49

I84733

gene CFTR protein - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999

C;Accession: I84733

R;Denamur, E.; Chehab, F.F.

Hum. Mol. Genet. 3, 1089-1094, 1994

A;Title: Analysis of the mouse and rat CFTR promoter regions.

A;Reference number: I49593; MUID:95072572; PMID:7526924

A;Accession: I84733

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-17 <RES>

A;Cross-references: GB:L26098; NID:g425185; PIDN:AAA73561.1; PID:g915270

C;Genetics:

A;Gene: CFTR

C;Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette homology

Query Match 45.2%; Score 19; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
|| ||  
Db 1 MQKSPL 6

RESULT 50

S05033

photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)

N;Alternate names: photosystem II 5K protein

C;Species: Synechococcus sp.

C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993

C;Accession: S05033

R;Ikeuchi, M.; Koike, H.; Inoue, Y.

FEBS Lett. 251, 155-160, 1989

A;Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II reaction center preparation.

A;Reference number: S05030

A;Accession: S05033

A;Molecule type: protein

A;Residues: 1-17 <IKE>

A;Note: the source is designated as Synechococcus vulcanus

C;Genetics:

A;Gene: psbL

C;Keywords: photosynthesis; photosystem II; thylakoid

Query Match 45.2%; Score 19; DB 2; Length 17;

Best Local Similarity 60.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5

|:| |

Db 1 MEPNP 5

Search completed: July 4, 2004, 04:47:12

Job time : 7.3806 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 13.7388 Seconds  
(without alignments)  
158.601 Million cell updates/sec

Title: US-09-641-802-1  
Perfect score: 42  
Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						



1	42	100.0	7	14	US-10-281-652-1	Sequence 1, Appli
2	33	78.6	10	14	US-10-161-791-278	Sequence 278, App
3	33	78.6	13	14	US-10-185-050-139	Sequence 139, App
4	32	76.2	9	9	US-09-835-232-11	Sequence 11, Appl
5	32	76.2	9	14	US-10-308-485-11	Sequence 11, Appl
6	32	76.2	10	14	US-10-185-050-141	Sequence 141, App
7	32	76.2	10	14	US-10-185-050-178	Sequence 178, App
8	32	76.2	11	9	US-09-835-232-8	Sequence 8, Appli
9	32	76.2	11	9	US-09-835-232-9	Sequence 9, Appli
10	32	76.2	11	14	US-10-308-485-8	Sequence 8, Appli
11	32	76.2	11	14	US-10-308-485-9	Sequence 9, Appli
12	32	76.2	12	10	US-09-845-612B-9	Sequence 9, Appli
13	32	76.2	12	14	US-10-161-791-251	Sequence 251, App
14	32	76.2	12	14	US-10-161-791-267	Sequence 267, App
15	32	76.2	13	10	US-09-945-917-13	Sequence 13, Appl
16	32	76.2	13	10	US-09-945-917-14	Sequence 14, Appl
17	32	76.2	13	10	US-09-945-917-19	Sequence 19, Appl
18	32	76.2	13	10	US-09-945-917-21	Sequence 21, Appl
19	32	76.2	13	10	US-09-845-917A-13	Sequence 13, Appl
20	32	76.2	13	10	US-09-845-917A-14	Sequence 14, Appl
21	32	76.2	13	10	US-09-845-917A-19	Sequence 19, Appl
22	32	76.2	13	10	US-09-845-917A-21	Sequence 21, Appl
23	32	76.2	13	14	US-10-067-668-11	Sequence 11, Appl
24	32	76.2	13	14	US-10-175-696-11	Sequence 11, Appl
25	32	76.2	14	9	US-09-879-957-186	Sequence 186, App
26	32	76.2	14	14	US-10-185-050-63	Sequence 63, Appl
27	32	76.2	14	14	US-10-148-936-3	Sequence 3, Appli
28	32	76.2	15	14	US-10-161-791-356	Sequence 356, App
29	32	76.2	15	14	US-10-161-791-385	Sequence 385, App
30	32	76.2	15	14	US-10-161-791-404	Sequence 404, App
31	32	76.2	15	14	US-10-161-791-414	Sequence 414, App
32	32	76.2	15	14	US-10-161-791-435	Sequence 435, App
33	32	76.2	15	14	US-10-161-791-436	Sequence 436, App
34	32	76.2	15	14	US-10-161-791-441	Sequence 441, App
35	32	76.2	15	14	US-10-161-791-452	Sequence 452, App
36	32	76.2	16	14	US-10-161-791-197	Sequence 197, App
37	32	76.2	17	14	US-10-161-791-360	Sequence 360, App
38	32	76.2	17	14	US-10-161-791-374	Sequence 374, App
39	32	76.2	18	14	US-10-161-791-320	Sequence 320, App
40	32	76.2	18	14	US-10-161-791-409	Sequence 409, App
41	31	73.8	12	14	US-10-235-175-16	Sequence 16, Appl
42	31	73.8	13	9	US-09-879-957-143	Sequence 143, App
43	31	73.8	13	14	US-10-185-050-8	Sequence 8, Appli
44	31	73.8	13	14	US-10-185-050-87	Sequence 87, Appl
45	31	73.8	14	12	US-10-393-815-235	Sequence 235, App
46	31	73.8	15	14	US-10-161-791-301	Sequence 301, App
47	31	73.8	16	14	US-10-161-791-344	Sequence 344, App
48	31	73.8	17	14	US-10-185-050-10	Sequence 10, Appl
49	30	71.4	10	14	US-10-062-710-77	Sequence 77, Appl
50	30	71.4	10	15	US-10-285-394-212	Sequence 212, App
51	30	71.4	12	12	US-10-609-217-312	Sequence 312, App
52	30	71.4	12	12	US-10-632-388-312	Sequence 312, App
53	30	71.4	12	12	US-10-651-723-312	Sequence 312, App
54	30	71.4	12	12	US-10-645-761-312	Sequence 312, App
55	30	71.4	12	14	US-10-158-596A-25	Sequence 25, Appl
56	30	71.4	12	14	US-10-157-775B-25	Sequence 25, Appl

57	30	71.4	12	14	US-10-185-050-135	Sequence 135, App
58	30	71.4	12	14	US-10-254-446A-25	Sequence 25, Appl
59	30	71.4	12	14	US-10-155-883B-25	Sequence 25, Appl
60	30	71.4	12	14	US-10-161-791-266	Sequence 266, App
61	30	71.4	12	16	US-10-666-696-312	Sequence 312, App
62	30	71.4	12	16	US-10-653-048-312	Sequence 312, App
63	30	71.4	13	14	US-10-156-932-75	Sequence 75, Appl
64	30	71.4	15	14	US-10-161-791-373	Sequence 373, App
65	30	71.4	15	14	US-10-161-791-382	Sequence 382, App
66	30	71.4	15	14	US-10-161-791-415	Sequence 415, App
67	30	71.4	15	14	US-10-161-791-430	Sequence 430, App
68	30	71.4	15	14	US-10-161-791-431	Sequence 431, App
69	30	71.4	15	15	US-10-328-916-58	Sequence 58, Appl
70	30	71.4	16	14	US-10-161-791-174	Sequence 174, App
71	30	71.4	16	14	US-10-161-791-199	Sequence 199, App
72	30	71.4	17	14	US-10-161-791-413	Sequence 413, App
73	29	69.0	8	14	US-10-193-709-8	Sequence 8, Appli
74	29	69.0	9	10	US-09-932-165-51	Sequence 51, Appl
75	29	69.0	9	10	US-09-932-165-1050	Sequence 1050, Ap
76	29	69.0	10	9	US-09-938-315-5	Sequence 5, Appli
77	29	69.0	10	10	US-09-932-165-152	Sequence 152, App
78	29	69.0	10	10	US-09-932-165-568	Sequence 568, App
79	29	69.0	10	14	US-10-161-791-5	Sequence 5, Appli
80	29	69.0	11	9	US-09-904-117-6	Sequence 6, Appli
81	29	69.0	11	14	US-10-161-791-261	Sequence 261, App
82	29	69.0	11	14	US-10-161-791-262	Sequence 262, App
83	29	69.0	11	14	US-10-161-791-290	Sequence 290, App
84	29	69.0	12	10	US-09-945-917-10	Sequence 10, Appl
85	29	69.0	12	10	US-09-945-917-22	Sequence 22, Appl
86	29	69.0	12	10	US-09-990-832C-84	Sequence 84, Appl
87	29	69.0	12	10	US-09-990-832C-96	Sequence 96, Appl
88	29	69.0	12	10	US-09-845-917A-10	Sequence 10, Appl
89	29	69.0	12	10	US-09-845-917A-22	Sequence 22, Appl
90	29	69.0	12	12	US-10-609-217-313	Sequence 313, App
91	29	69.0	12	12	US-10-632-388-313	Sequence 313, App
92	29	69.0	12	12	US-10-651-723-313	Sequence 313, App
93	29	69.0	12	12	US-10-645-761-313	Sequence 313, App
94	29	69.0	12	14	US-10-185-050-154	Sequence 154, App
95	29	69.0	12	14	US-10-161-791-268	Sequence 268, App
96	29	69.0	12	14	US-10-161-791-269	Sequence 269, App
97	29	69.0	12	15	US-10-418-751-47	Sequence 47, Appl
98	29	69.0	12	15	US-10-418-752-47	Sequence 47, Appl
99	29	69.0	12	16	US-10-666-696-313	Sequence 313, App
100	29	69.0	12	16	US-10-653-048-313	Sequence 313, App

#### ALIGNMENTS

##### RESULT 1

US-10-281-652-1

; Sequence 1, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

```

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-1

```

```

Query Match          100.0%; Score 42; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 MQPPPLP 7
        |||||
Db      1 MQPPPLP 7

```

#### RESULT 2

```

US-10-161-791-278
; Sequence 278, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-278

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Query Match          78.6%; Score 33; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches    5; Conservative    1; Mismatches    0; Indels    0; Gaps    0;

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Qy      2 QPPPLP 7
        :|||||
Db      1 KPPPLP 6

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RESULT 3

US-10-185-050-139

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; Sequence 139, Application US/10185050
; Publication No. US20030077577A1

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GENERAL INFORMATION:

```

; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME

```

```

; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050

```

```

;          FILING DATE: 28-Jun-2002
;          CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/826,516
;          FILING DATE: 03-Apr-1997
;          ATTORNEY/AGENT INFORMATION:
;          NAME: MISROCK, S. LESLIE
;          REGISTRATION NUMBER: 18,872
;          REFERENCE/DOCKET NUMBER: 1101-208-999
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 896-8864/9741
;          TELEX: 66141 PENNIE
;          INFORMATION FOR SEQ ID NO: 139:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 13 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: <Unknown>
;          TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 139:
US-10-185-050-139

```

```

Query Match          78.6%;  Score 33;  DB 14;  Length 13;
Best Local Similarity 71.4%;  Pred. No. 3.2e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

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```

QY          1 MQPPPLP 7
             :||| |
Db          2 VQPPAP 8

```

```

RESULT 4
US-09-835-232-11
; Sequence 11, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-835-232-11

```

```

Query Match          76.2%;  Score 32;  DB 9;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.2e+06;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

Qy 3 PPPLP 7  
|||||  
Db 4 PPPLP 8

RESULT 5

US-10-308-485-11

; Sequence 11, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/10/308,485  
; CURRENT FILING DATE: 2002-12-03  
; PRIOR APPLICATION NUMBER: US/09/835,232  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-308-485-11

Query Match 76.2%; Score 32; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 4 PPPLP 8

RESULT 6

US-10-185-050-141

; Sequence 141, Application US/10185050  
; Publication No. US20030077577A1  
; GENERAL INFORMATION:  
; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.  
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME  
; NUMBER OF SEQUENCES: 233  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

```

;           ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/185,050
;           FILING DATE: 28-Jun-2002
;           CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/826,516
;           FILING DATE: 03-Apr-1997
;   ATTORNEY/AGENT INFORMATION:
;           NAME: MISROCK, S. LESLIE
;           REGISTRATION NUMBER: 18,872
;           REFERENCE/DOCKET NUMBER: 1101-208-999
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 896-8864/9741
;           TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 141:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 10 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-185-050-141

```

```

Query Match          76.2%; Score 32; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          5 PPPLP 9

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# RESULT 7

US-10-185-050-178

; Sequence 178, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

```

;          COUNTRY: USA
;          ZIP: 10036-2711
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/185,050
;          FILING DATE: 28-Jun-2002
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/826,516
;          FILING DATE: 03-Apr-1997
;    ATTORNEY/AGENT INFORMATION:
;          NAME: MISROCK, S. LESLIE
;          REGISTRATION NUMBER: 18,872
;          REFERENCE/DOCKET NUMBER: 1101-208-999
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 896-8864/9741
;          TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 178:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-10-185-050-178

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Query Match      76.2%;  Score 32;  DB 14;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 3.4e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      5 PPPLP 9

```

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RESULT 8
US-09-835-232-8
; Sequence 8, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0

```



; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 1  
; OTHER INFORMATION: Xaa=Met or Val  
US-09-835-232-8

Query Match 76.2%; Score 32; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 6 PPPLP 10

RESULT 9

US-09-835-232-9

; Sequence 9, Application US/09835232  
; Patent No. US20020098489A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin  
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 00383/052002  
; CURRENT APPLICATION NUMBER: US/09/835,232  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/196,811  
; PRIOR FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-835-232-9

Query Match 76.2%; Score 32; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 7 PPPLP 11

RESULT 10

US-10-308-485-8

; Sequence 8, Application US/10308485  
; Publication No. US20030170683A1  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Leader, Benjamin

```

; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION:  AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa=Met or Val
US-10-308-485-8

```

```

Query Match          76.2%; Score 32; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 PPPLP 7
        |||||
Db      6 PPPLP 10

```

# RESULT 11

```

US-10-308-485-9
; Sequence 9, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION:  AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-308-485-9

```

```

Query Match          76.2%; Score 32; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 3 PPPLP 7  
 ||||  
Db 7 PPPLP 11

RESULT 12

US-09-845-612B-9

; Sequence 9, Application US/09845612B  
; Publication No. US20030083261A1  
; GENERAL INFORMATION:  
; APPLICANT: YU, HONGTAO  
; APPLICANT: TANG, ZHANYUN  
; APPLICANT: LUO, XUELIAN  
; APPLICANT: RIZO-REY, JOSE  
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF  
THE MITOTIC CHECK  
; TITLE OF INVENTION: POINT PROTEIN MAD2  
; FILE REFERENCE: UTSD:795  
; CURRENT APPLICATION NUMBER: US/09/845,612B  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(12)  
; OTHER INFORMATION: synthetic peptide  
US-09-845-612B-9

Query Match 76.2%; Score 32; DB 10; Length 12;  
Best Local Similarity 83.3%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
 :||||  
Db 5 LQPPPL 10

RESULT 13

US-10-161-791-251

; Sequence 251, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 251:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-251

```

```

Query Match          76.2%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          6 PPPLP 10

```

# RESULT 14

US-10-161-791-267

```

; Sequence 267, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

```

```

; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 267:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-267

```

```

Query Match          76.2%; Score 32; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          6 PPPLP 10

```

# RESULT 15

US-09-945-917-13

; Sequence 13, Application US/09945917

; Publication No. US20030042381A1

## ; GENERAL INFORMATION:

; APPLICANT: Bogaert, Thierry

; APPLICANT: Vandekerckhove, Joel

; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH

; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR

; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR

; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-13

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | | |  
Db 5 PPPLP 9

RESULT 16

US-09-945-917-14

; Sequence 14, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/945,917  
; CURRENT FILING DATE: 1998-09-21  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-945-917-14

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 57.1%; Pred. No. 4.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
: | | | : |  
Db 3 LSPPPIP 9

RESULT 17

US-09-945-917-19

; Sequence 19, Application US/09945917  
; Publication No. US20030042381A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry

```
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-19
```

```
Query Match          76.2%; Score 32; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY          3 PPPLP 7
             |||||
Db          6 PPPLP 10
```

#### RESULT 18

```
US-09-945-917-21
; Sequence 21, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-21
```

```
Query Match          76.2%; Score 32; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY          3 PPPLP 7
             |||||
Db          5 PPPLP 9
```

#### RESULT 19

US-09-845-917A-13

; Sequence 13, Application US/09845917A  
; Publication No. US20030167538A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-845-917A-13

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | |  
Db 5 PPPLP 9

RESULT 20

US-09-845-917A-14

; Sequence 14, Application US/09845917A  
; Publication No. US20030167538A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-845-917A-14

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 57.1%; Pred. No. 4.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7



: |||:|  
Db                  3 LSPPPIP 9

RESULT 21

US-09-845-917A-19

; Sequence 19, Application US/09845917A  
; Publication No. US20030167538A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-845-917A-19

Query Match                  76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity      100.0%; Pred. No. 4.3e+02;  
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy                  3 PPPLP 7  
                  |||||  
Db                  6 PPPLP 10

RESULT 22

US-09-845-917A-21

; Sequence 21, Application US/09845917A  
; Publication No. US20030167538A1  
; GENERAL INFORMATION:  
; APPLICANT: Bogaert, Thierry  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTIANING THEM AND THEIR  
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
; FILE REFERENCE: P/14-1  
; CURRENT APPLICATION NUMBER: US/09/845,917A  
; CURRENT FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-845-917A-21

Query Match 76.2%; Score 32; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 5 PPPLP 9

RESULT 23

US-10-067-668-11

; Sequence 11, Application US/10067668  
; Publication No. US20030022334A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN  
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-136001  
; CURRENT APPLICATION NUMBER: US/10/067,668  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
US-10-067-668-11

Query Match 76.2%; Score 32; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 4 PPPLP 8

RESULT 24

US-10-175-696-11

; Sequence 11, Application US/10175696  
; Publication No. US20030092658A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10/175,696  
; CURRENT FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 10/067,668  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02

```

; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: consensus sequence
US-10-175-696-11

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 13;
Best Local Similarity 100.0%;  Pred. No. 4.3e+02;
Matches      5;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      4 PPPLP 8

```

RESULT 25

US-09-879-957-186

; Sequence 186, Application US/09879957

; Patent No. US20020034755A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; HOFFMAN, No. US20020034755A1h

; KAY, Brian K.

; FOWLKES, Dana M.

; McCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

```

;           ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/879,957
;           FILING DATE: 13-Jun-2001
;           CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/630,915
;           FILING DATE: 03-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;           NAME: Misrock, S. Leslie
;           REGISTRATION NUMBER: 18,872
;           REFERENCE/DOCKET NUMBER: 1101-174
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 790-9090
;           TELEFAX: (212) 869-8864/9741
;           TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 186:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 14 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: unknown
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-09-879-957-186

```

```

Query Match          76.2%;  Score 32;  DB 9;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 4.5e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
             |||||
Db          5 PPPLP 9

```

# RESULT 26

US-10-185-050-63

; Sequence 63, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

```

;          COUNTRY: USA
;          ZIP: 10036-2711
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/185,050
;          FILING DATE: 28-Jun-2002
;          CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/826,516
;          FILING DATE: 03-Apr-1997
;    ATTORNEY/AGENT INFORMATION:
;          NAME: MISROCK, S. LESLIE
;          REGISTRATION NUMBER: 18,872
;          REFERENCE/DOCKET NUMBER: 1101-208-999
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 790-9090
;          TELEFAX: (212) 896-8864/9741
;          TELEX: 66141 PENNIE
;    INFORMATION FOR SEQ ID NO: 63:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 14 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: unknown
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-185-050-63

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 14;
Best Local Similarity 100.0%;  Pred. No. 4.5e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          5 PPPLP 9

```

# RESULT 27

US-10-148-936-3

```

; Sequence 3, Application US/10148936
; Publication No. US20030113819A1
; GENERAL INFORMATION:
; APPLICANT: Horton, Jeffrey
; APPLICANT: Smith, John
; APPLICANT: Teear, Michelle
; APPLICANT: Kendall, Jonathan
; APPLICANT: Michael, Nigel
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells
; FILE REFERENCE: PA9963
; CURRENT APPLICATION NUMBER: US/10/148,936
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04593
; PRIOR FILING DATE: 2000-12-04

```

; PRIOR APPLICATION NUMBER: GB 9928674.2  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligomer  
US-10-148-936-3

Query Match 76.2%; Score 32; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||||  
Db 5 PPPLP 9

RESULT 28

US-10-161-791-356

; Sequence 356, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie

```

;     REGISTRATION NUMBER:  18,872
;     REFERENCE/DOCKET NUMBER:  1101-202
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 790-9090
;     TELEFAX:  (212) 869-9741/8864
;     TELEX:  66141 PENNIE
;     INFORMATION FOR SEQ ID NO:  356:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH:  15 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
US-10-161-791-356

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 4.8e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          3 PPPLP 7
            |||||
Db          7 PPPLP 11

```

# RESULT 29

US-10-161-791-385

; Sequence 385, Application US/10161791

; Publication No. US20030186863A1

## ; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Misrock, S. Leslie
;   REGISTRATION NUMBER: 18,872
;   REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 790-9090
;   TELEFAX: (212) 869-9741/8864
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 15 amino acids
;     TYPE: amino acid
;     TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-10-161-791-385

```

```

Query Match          76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      7 PPPLP 11

```

RESULT 30

US-10-161-791-404

```

; Sequence 404, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
;   APPLICANT: SPARKS, Andrew B.
;   APPLICANT: KAY, Brian K.
;   APPLICANT: THORN, Judith M.
;   APPLICANT: QUILLIAM, Lawrence A.
;   APPLICANT: DER, Channing J.
;   APPLICANT: FOWLKES, Dana M.
;   APPLICANT: RIDER, James E.
;   TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION: ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES: 467
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: U.S.A.
;     ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/161,791
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:

```



```

; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-404

```

```

Query Match          76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 PPPLP 7
        |||||
Db      4 PPPLP 8

```

RESULT 31

US-10-161-791-414

```

; Sequence 414, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-414

```

```

Query Match          76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      4 PPPLP 8

```

# RESULT 32

```

US-10-161-791-435
; Sequence 435, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 435:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-435

```

```

Query Match          76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      4 PPPLP 8

```

RESULT 33

US-10-161-791-436

```

; Sequence 436, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/161,791
;      FILING DATE:
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,999
;      FILING DATE:  16-FEB-1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;      INFORMATION FOR SEQ ID NO:  436:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
US-10-161-791-436

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 15;
Best Local Similarity  57.1%;  Pred. No. 4.8e+02;
Matches      4;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

```

```

Qy      1 MQPPPLP 7
        : |||:|
Db      2 LSPPPIP 8

```

#### RESULT 34

US-10-161-791-441

```

; Sequence 441, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk

```

```

;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/161,791
;      FILING DATE:
;      CLASSIFICATION:
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,999
;      FILING DATE:  16-FEB-1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  1101-202
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;      INFORMATION FOR SEQ ID NO:  441:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
US-10-161-791-441

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 4.8e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          5 PPPLP 9

```

# RESULT 35

US-10-161-791-452

```

; Sequence 452, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
;   APPLICANT:  SPARKS, Andrew B.
;   APPLICANT:  KAY, Brian K.
;   APPLICANT:  THORN, Judith M.
;   APPLICANT:  QUILLIAM, Lawrence A.
;   APPLICANT:  DER, Channing J.
;   APPLICANT:  FOWLKES, Dana M.
;   APPLICANT:  RIDER, James E.
;   TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;   TITLE OF INVENTION:  ISOLATING AND USING SAME
;   NUMBER OF SEQUENCES:  467
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-452

```

```

Query Match          76.2%; Score 32; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 PPPLP 7
        |||||
Db      7 PPPLP 11

```

# RESULT 36

US-10-161-791-197

```

; Sequence 197, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-197

```

```

Query Match          76.2%; Score 32; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          9 PPPLP 13

```

# RESULT 37

US-10-161-791-360

; Sequence 360, Application US/10161791

; Publication No. US20030186863A1

## ; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

```

;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;  COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/161,791
;      FILING DATE:
;      CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,999
;      FILING DATE:  16-FEB-1996
;  ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  1101-202
;  TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  360:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
US-10-161-791-360

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 17;
Best Local Similarity 100.0%;  Pred. No. 5.4e+02;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          9 PPPLP 13

```

# RESULT 38

US-10-161-791-374

```

; Sequence 374, Application US/10161791
; Publication No. US20030186863A1
;  GENERAL INFORMATION:
;      APPLICANT:  SPARKS, Andrew B.
;      APPLICANT:  KAY, Brian K.
;      APPLICANT:  THORN, Judith M.
;      APPLICANT:  QUILLIAM, Lawrence A.
;      APPLICANT:  DER, Channing J.
;      APPLICANT:  FOWLKES, Dana M.
;      APPLICANT:  RIDER, James E.
;      TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
;      TITLE OF INVENTION:  ISOLATING AND USING SAME
;      NUMBER OF SEQUENCES:  467
;      CORRESPONDENCE ADDRESS:

```



; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/161,791  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/602,999  
 ; FILING DATE: 16-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Misrock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 1101-202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 374:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 US-10-161-791-374

Query Match 76.2%; Score 32; DB 14; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 |||||  
 Db 9 PPPLP 13

# RESULT 39

US-10-161-791-320

; Sequence 320, Application US/10161791  
 ; Publication No. US20030186863A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SPARKS, Andrew B.  
 ; APPLICANT: KAY, Brian K.  
 ; APPLICANT: THORN, Judith M.  
 ; APPLICANT: QUILLIAM, Lawrence A.  
 ; APPLICANT: DER, Channing J.  
 ; APPLICANT: FOWLKES, Dana M.  
 ; APPLICANT: RIDER, James E.  
 ; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
 ; TITLE OF INVENTION: ISOLATING AND USING SAME

```

; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-320

```

```

Query Match          76.2%; Score 32; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches    5; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          3 PPPLP 7
             |||||
Db          10 PPPLP 14

```

```

RESULT 40
US-10-161-791-409
; Sequence 409, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.

```

```

; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/10/161,791
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/602,999
;   FILING DATE:  16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  409:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  18 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-10-161-791-409

```

```

Query Match          76.2%;  Score 32;  DB 14;  Length 18;
Best Local Similarity 100.0%;  Pred. No. 5.6e+02;
Matches      5;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          3 PPPLP 7
            |||||
Db          11 PPPLP 15

```

```

RESULT 41
US-10-235-175-16
; Sequence 16, Application US/10235175
; Publication No. US20030166287A1
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmuth
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID
; TITLE OF INVENTION:  TRANSPORTER

```

```

; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/10/235,175
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US/09/315,926
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage display
; OTHER INFORMATION: peptide
US-10-235-175-16

```

```

Query Match          73.8%; Score 31; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches      4; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      1 MQPPPLP 7
        : |||:|
Db      2 LMPPVP 8

```

#### RESULT 42

US-09-879-957-143

; Sequence 143, Application US/09879957

; Patent No. US20020034755A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; HOFFMAN, No. US20020034755A1h

; KAY, Brian K.

; FOWLKES, Dana M.

; McCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

```

;      APPLICATION NUMBER: US/09/879,957
;      FILING DATE: 13-Jun-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 08/630,915
;      FILING DATE: 03-APR-1996
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Misrock, S. Leslie
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-174
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-8864/9741
;      TELEX: 66141 PENNIE
;
;      INFORMATION FOR SEQ ID NO: 143:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 13 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: <Unknown>
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 143:
US-09-879-957-143

```

```

Query Match          73.8%;  Score 31;  DB 9;  Length 13;
Best Local Similarity 71.4%;  Pred. No. 5.8e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

```

```

Qy      1 MQPPPLP 7
        :|||| |
Db      2 VQPPPPP 8

```

#### RESULT 43

US-10-185-050-8

```

; Sequence 8, Application US/10185050
; Publication No. US20030077577A1
;   GENERAL INFORMATION:
;   APPLICANT: Pirozzi, Gregorio
;               Kay, Brian K.
;               Fowlkes, Dana M.
;   TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
;                       POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING
SAME
;   NUMBER OF SEQUENCES: 233
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: PENNIE & EDMONDS LLP
;       STREET: 1155 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10036-2711
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-185-050-8

```

```

Query Match          73.8%; Score 31; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 5.8e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MQPPPLP 7
        :|||| |
Db      2 VQPPPPP 8

```

#### RESULT 44

US-10-185-050-87

; Sequence 87, Application US/10185050

; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio

; Kay, Brian K.

; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING

SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/185,050
;      FILING DATE: 28-Jun-2002
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/08/826,516
;      FILING DATE: 03-Apr-1997
;      ATTORNEY/AGENT INFORMATION:
;      NAME: MISROCK, S. LESLIE
;      REGISTRATION NUMBER: 18,872
;      REFERENCE/DOCKET NUMBER: 1101-208-999
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 896-8864/9741
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 87:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 13 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: <Unknown>
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-10-185-050-87

```

```

Query Match          73.8%;  Score 31;  DB 14;  Length 13;
Best Local Similarity 71.4%;  Pred. No. 5.8e+02;
Matches      5;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

```

```

Qy      1 MQPPPLP 7
        :|||| |
Db      2 VQPPPPP 8

```

#### RESULT 45

US-10-393-815-235

```

; Sequence 235, Application US/10393815
; Publication No. US20030224413A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms
; TITLE OF INVENTION: And Methods of Use Thereof
; FILE REFERENCE: 15966-534B
; CURRENT APPLICATION NUMBER: US/10/393,815
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 235
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT

```

; LOCATION: (7)...(0)  
; OTHER INFORMATION: cSNP translation  
US-10-393-815-235

Query Match 73.8%; Score 31; DB 12; Length 14;  
Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:|||||  
Db 3 EPPVP 8

RESULT 46

US-10-161-791-301

; Sequence 301, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 301:  
; SEQUENCE CHARACTERISTICS:



;     LENGTH: 15 amino acids  
;     TYPE: amino acid  
;     TOPOLOGY: unknown  
;     MOLECULE TYPE: peptide  
US-10-161-791-301

Query Match           73.8%;   Score 31;   DB 14;   Length 15;  
Best Local Similarity   83.3%;   Pred. No. 6.5e+02;  
Matches     5;   Conservative     0;   Mismatches     1;   Indels     0;   Gaps     0;

Qy           2 QPPPLP 7  
             | | | | |  
Db           1 QPPPRP 6

RESULT 47

US-10-161-791-344

; Sequence 344, Application US/10161791

; Publication No. US20030186863A1

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/161,791

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 344:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-344

Query Match 73.8%; Score 31; DB 14; Length 16;  
Best Local Similarity 71.4%; Pred. No. 6.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
|:| | | |  
Db 2 MRPPPPP 8

RESULT 48

US-10-185-050-10

; Sequence 10, Application US/10185050  
; Publication No. US20030077577A1

; GENERAL INFORMATION:

; APPLICANT: Pirozzi, Gregorio  
; Kay, Brian K.  
; Fowlkes, Dana M.

; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING  
SAME

; NUMBER OF SEQUENCES: 233

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050  
; FILING DATE: 28-Jun-2002  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516  
; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-208-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 896-8864/9741  
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-185-050-10

Query Match 73.8%; Score 31; DB 14; Length 17;  
Best Local Similarity 71.4%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
:|||||  
Db 6 VQPPPPP 12

RESULT 49

US-10-062-710-77

; Sequence 77, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; TITLE OF INVENTION: Via Peptide Vaccines  
; FILE REFERENCE: 3781-001-27  
; CURRENT APPLICATION NUMBER: US/10/062,710  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 77  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV CTL-Epitopes  
US-10-062-710-77

Query Match 71.4%; Score 30; DB 14; Length 10;  
Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||:  
Db 1 PPPIP 5

RESULT 50

US-10-285-394-212

; Sequence 212, Application US/10285394  
; Publication No. US20030228583A1

; GENERAL INFORMATION:  
; APPLICANT: AMACHER, DAVID E.  
; APPLICANT: FASULO, LISA M.  
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
; APPLICANT: HOLT, GORDON DUANE  
; APPLICANT: STIGER, THOMAS R.  
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
; FILE REFERENCE: POA-003.01  
; CURRENT APPLICATION NUMBER: US/10/285,394  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,964  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 212  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-285-394-212

Query Match 71.4%; Score 30; DB 15; Length 10;  
Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
|||:|  
Db 5 PPPIP 9

Search completed: July 4, 2004, 05:12:21  
Job time : 15.7388 secs

OM protein - protein search, using sw model

<div> <div>Result</div> <div>Query</div> </div>						
No.	Score	Match	Length	DB	ID	Description

1	26	61.9	18	4	Q9UCT9	Q9uct9 homo sapien
2	25	59.5	15	10	P82439	P82439 nicotiana t
3	25	59.5	17	10	Q41400	Q41400 sesbania ro
4	25	59.5	18	12	Q84129	Q84129 influenzavi
5	24	57.1	9	5	Q9TWV0	Q9twv0 anthopleura
6	23	54.8	16	6	Q9TQZ7	Q9tqz7 bos taurus
7	23	54.8	17	4	Q9NQY8	Q9nqy8 homo sapien
8	22	52.4	14	2	P81715	P81715 streptomyce
9	22	52.4	16	6	Q9TRR1	Q9trr1 oryctolagus
10	22	52.4	17	13	Q90XE2	Q90xe2 gallus gall
11	21	50.0	10	12	Q9Q0W9	Q9q0w9 polyomaviru
12	21	50.0	10	12	Q8JV70	Q8jv70 polyomaviru
13	21	50.0	10	12	Q9Q0W1	Q9q0w1 polyomaviru
14	21	50.0	10	12	Q8JV68	Q8jv68 polyomaviru
15	21	50.0	10	12	Q9Q0V9	Q9q0v9 polyomaviru
16	21	50.0	10	12	Q9Q0W7	Q9q0w7 polyomaviru
17	21	50.0	10	12	Q8JV66	Q8jv66 polyomaviru
18	21	50.0	10	12	Q9Q0V7	Q9q0v7 polyomaviru
19	21	50.0	10	12	Q8JV82	Q8jv82 polyomaviru
20	21	50.0	10	12	Q8JV76	Q8jv76 polyomaviru
21	21	50.0	10	12	Q8JV74	Q8jv74 polyomaviru
22	21	50.0	10	12	Q9Q0W5	Q9q0w5 polyomaviru
23	21	50.0	10	12	Q9Q0X3	Q9q0x3 polyomaviru
24	21	50.0	10	12	Q9Q0X5	Q9q0x5 polyomaviru
25	21	50.0	10	12	Q9Q0W3	Q9q0w3 polyomaviru
26	21	50.0	10	12	Q8JV80	Q8jv80 polyomaviru
27	21	50.0	10	12	Q9Q0X1	Q9q0x1 polyomaviru
28	21	50.0	10	12	Q9Q0X9	Q9q0x9 polyomaviru
29	21	50.0	10	12	Q8JV72	Q8jv72 polyomaviru
30	21	50.0	11	10	P82436	P82436 nicotiana t
31	21	50.0	11	13	Q8UUP1	Q8uup1 xenopus lae
32	21	50.0	12	4	Q9BZ49	Q9bz49 homo sapien
33	21	50.0	12	10	Q93X21	Q93x21 zea mays (m
34	21	50.0	15	4	Q9UCC2	Q9ucc2 homo sapien
35	21	50.0	15	6	Q9TR14	Q9trl4 bos taurus
36	21	50.0	15	10	Q9S8N8	Q9s8n8 hordeum vul
37	21	50.0	17	4	Q14001	Q14001 homo sapien
38	21	50.0	17	6	Q9TR22	Q9tr22 bos taurus
39	21	50.0	17	10	O49225	O49225 glycine max
40	21	50.0	18	4	Q8NFB4	Q8nfb4 homo sapien
41	21	50.0	18	4	Q9H1I3	Q9h1i3 homo sapien
42	21	50.0	18	11	Q9JIE9	Q9jie9 mus musculu
43	21	50.0	18	13	Q8QFT3	Q8qft3 gallus gall
44	20	47.6	9	4	Q9UCS8	Q9ucs8 homo sapien
45	20	47.6	11	4	Q8IVG8	Q8ivg8 homo sapien
46	20	47.6	12	10	P82441	P82441 nicotiana t
47	20	47.6	13	12	Q67604	Q67604 squash leaf
48	20	47.6	16	4	Q9UQS4	Q9uqs4 homo sapien
49	20	47.6	16	10	Q8RVF4	Q8rvf4 zea mays (m
50	20	47.6	17	4	Q96P96	Q96p96 homo sapien
51	19.5	46.4	17	6	Q9TR78	Q9tr78 didelphis m
52	19	45.2	9	4	Q9UMF3	Q9umf3 homo sapien
53	19	45.2	9	10	P82429	P82429 nicotiana t
54	19	45.2	10	10	P81898	P81898 prunus dulc
55	19	45.2	11	11	Q80WI1	Q80wil mus sp. nt-
56	19	45.2	12	10	P82328	P82328 pisum sativ
57	19	45.2	13	2	Q50476	Q50476 mycobacteri

58	19	45.2	13	16	Q8X4F5	Q8x4f5 escherichia
59	19	45.2	16	4	Q9UC52	Q9uc52 homo sapien
60	19	45.2	16	11	Q9QUW5	Q9quw5 rattus sp.
61	19	45.2	16	13	Q9PRU6	Q9pru6 gallus gall
62	19	45.2	17	2	Q9R5J3	Q9r5j3 mycoplasma
63	19	45.2	17	13	Q9PRU7	Q9pru7 gallus gall
64	19	45.2	18	4	Q16053	Q16053 homo sapien
65	19	45.2	18	6	P79214	P79214 oryctolagus
66	19	45.2	18	11	P97522	P97522 rattus norv
67	19	45.2	18	13	Q90790	Q90790 gallus gall
68	18.5	44.0	17	13	Q9PS39	Q9ps39 carassius a
69	18	42.9	9	2	P83157	P83157 anabaena sp
70	18	42.9	9	10	Q9S8J8	Q9s8j8 oryza sativ
71	18	42.9	10	4	Q9UE86	Q9ue86 homo sapien
72	18	42.9	10	11	Q9QVF7	Q9qvf7 rattus sp.
73	18	42.9	10	11	Q8VHM9	Q8vhm9 mus musculu
74	18	42.9	11	4	Q9HCN5	Q9hcn5 homo sapien
75	18	42.9	12	2	Q8KZ86	Q8kz86 acinetobact
76	18	42.9	12	6	P83127	P83127 bos indicus
77	18	42.9	13	4	Q9UEE2	Q9uee2 homo sapien
78	18	42.9	13	4	Q14182	Q14182 homo sapien
79	18	42.9	13	4	Q14890	Q14890 homo sapien
80	18	42.9	13	11	O88176	O88176 mus musculu
81	18	42.9	14	10	P82326	P82326 pisum sativ
82	18	42.9	14	12	Q8V3U6	Q8v3u6 tomato yell
83	18	42.9	15	3	Q9UR63	Q9ur63 emericella
84	18	42.9	15	10	Q40562	Q40562 nicotiana t
85	18	42.9	15	10	Q40563	Q40563 nicotiana t
86	18	42.9	16	4	Q9NNZ2	Q9nnz2 homo sapien
87	18	42.9	16	5	Q9TWN7	Q9tnw7 toxoplasma
88	18	42.9	16	6	Q9BGG8	Q9bgg8 sores arane
89	18	42.9	16	12	Q83967	Q83967 influenzavi
90	18	42.9	16	12	Q83960	Q83960 influenzavi
91	18	42.9	16	12	Q84055	Q84055 influenzavi
92	18	42.9	16	15	Q8J699	Q8j699 human t-lym
93	18	42.9	16	15	Q8J6A6	Q8j6a6 human t-lym
94	18	42.9	16	15	Q8J6I4	Q8j6i4 human t-lym
95	18	42.9	16	15	Q8J6A1	Q8j6a1 human t-lym
96	18	42.9	16	15	Q8J6A3	Q8j6a3 human t-lym
97	18	42.9	16	15	Q8J697	Q8j697 human t-lym
98	18	42.9	16	15	Q8J6A0	Q8j6a0 human t-lym
99	18	42.9	16	15	Q8J6A5	Q8j6a5 human t-lym
100	18	42.9	16	15	Q8J6A2	Q8j6a2 human t-lym

# ALIGNMENTS

## RESULT 1

Q9UCT9

ID Q9UCT9 PRELIMINARY; PRT; 18 AA.

AC Q9UCT9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE PRG=PROLINE-rich glycoprotein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373355; PubMed=1894623;  
 RA Gillece-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,  
 RA Fisher S.J.;  
 RT "Structure and bacterial receptor activity of a human salivary  
 RT proline-rich glycoprotein.";  
 RL J. Biol. Chem. 266:17358-17368(1991).  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0008368; F:Gram-negative bacterial binding; NAS.  
 DR GO; GO:0009618; P:response to pathogenic bacteria; NAS.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 61.9%; Score 26; DB 4; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 ||| |  
 Db 4 PPPRP 8

## RESULT 2

P82439

ID P82439 PRELIMINARY; PRT; 15 AA.  
 AC P82439;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 200 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall; Hydroxylation.  
 FT MOD\_RES 6 6 HYDROXYLATION.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 59.5%; Score 25; DB 10; Length 15;



Best Local Similarity 80.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
||| |  
Db 6 PPPPP 10

RESULT 3

Q41400

ID Q41400 PRELIMINARY; PRT; 17 AA.  
AC Q41400;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hydroxyproline-rich protein (Fragment).  
OS Sesbania rostrata.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.  
OX NCBI\_TaxID=3895;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sesbania rostrata;  
RC TISSUE=Bacterial infected stem located root primordia;  
RX MEDLINE=96112737; PubMed=8664492;  
RA Goormachtig S., Valerio-Lepiniec M., Szczygłowski K., Van Montagu M.,  
RA Holsters M., De Bruijn F.;  
RT "Use of differential display to identify novel Sesbania rostrata genes  
RT enhanced by Azorhizobium caulinodans infection."  
RL Mol. Plant Microbe Interact. 8:816-824(1995).  
DR EMBL; Z48673; CAA88592.1; -.  
DR PIR; S57991; S57991.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 59.5%; Score 25; DB 10; Length 17;  
Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
||| |  
Db 10 PPPPP 14

RESULT 4

Q84129

ID Q84129 PRELIMINARY; PRT; 18 AA.  
AC Q84129;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg  
DE 8), COOH terminus of NS1 (Fragment).  
OS Influenzavirus A.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses.

OX NCBI\_TaxID=197911;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83303830; PubMed=6612993;  
 RA Parvin J.D., Young J.F., Palese P.;  
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural  
 RT proteins of influenza a virus isolates.";  
 RL Virology 128:512-517(1983).  
 DR EMBL; K00959; AAA43541.1; -.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR Pfam; PF00600; Flu\_NS1; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;

Query Match 59.5%; Score 25; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
 ||||  
 Db 11 PPLP 14

#### RESULT 5

Q9TWV0

ID Q9TWV0 PRELIMINARY; PRT; 9 AA.  
 AC Q9TWV0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Antho-RPAMIDE=NEUROPEPTIDE.  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93126143; PubMed=1480510;  
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;  
 RT "Isolation of Leu-Pro-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),  
 RT an N-terminally protected, biologically active neuropeptide from sea  
 RT anemones.";  
 RL Peptides 13:851-857(1992).  
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 57.1%; Score 24; DB 5; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1e+06;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 : | |||  
 Db 1 LPPGPLP 7

#### RESULT 6

Q9TQZ7

ID Q9TQZ7 PRELIMINARY; PRT; 16 AA.  
AC Q9TQZ7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Factor H (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96202005; PubMed=8615824;  
RA Soames C.J., Day A.J., Sim R.B.;  
RT "Prediction from sequence comparisons of residues of factor H involved  
in the interaction with complement component C3b.";  
RL Biochem. J. 315:523-531(1996).  
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 54.8%; Score 23; DB 6; Length 16;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPPP 5  
:| | |  
Db 5 EPPP 8

#### RESULT 7

Q9NQY8

ID Q9NQY8 PRELIMINARY; PRT; 17 AA.  
AC Q9NQY8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Transcription factor 12 (Fragment).  
GN TCF12.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gan T.-I., O'Sickey T., Zhang Y., Kim U.-J., Bina M.;  
RT "Organization of the HTF4 Gene.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF271610; AAF82574.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1802 MW; E26E7FB1D7903679 CRC64;

Query Match 54.8%; Score 23; DB 4; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7

Db            || ||  
             11 PPGLP 15

RESULT 8

P81715

ID    P81715            PRELIMINARY;            PRT;        14 AA.  
AC    P81715;  
DT    01-JUN-2001 (TrEMBLrel. 17, Created)  
DT    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    Leupeptin-inactivating enzyme (EC 3.4.24.-) (LIE) (Fragment).  
OS    Streptomyces exfoliatus (Streptomyces hydrogenans).  
OC    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC    Streptomycineae; Streptomycetaceae; Streptomyces.  
OX    NCBI\_TaxID=1905;  
RN    [1]  
RP    SEQUENCE.  
RC    STRAIN=SMF13;  
RX    PubMed=9531495;  
RA    Kim I.S., Kim Y.B., Lee K.J.;  
RT    "Characterization of the leupeptin-inactivating enzyme from  
RT    Streptomyces exfoliatus SMF13 which produces leupeptin."  
RL    Biochem. J. 331:539-545(1998).  
CC    -!- FUNCTION: A LEUCINE-SPECIFIC METALLOPROTEASE THAT PLAYS A ROLE IN  
CC        CONTROLLING THE AMOUNT OF LEUPEPTIN DURING COLONY DEVELOPMENT.  
CC        OPTIMUM PH IS 9.0 AND TEMPERATURE IS 40 DEGREES CELSIUS.  
CC    -!- FUNCTION: DEGRADES LEUPEPTIN INTO THREE COMPONENTS, ACETYL-  
CC        LEUCINE, LEUCINE AND ARGININAL.  
CC    -!- CATALYTIC ACTIVITY: HAS A STRICT PREFERENCE FOR LEUCINE AT THE P1  
CC        SITE.  
CC    -!- ENZYME REGULATION: ACTIVITY IS INHIBITED BY METALLOPROTEASE  
CC        INHIBITORS AND ACTIVATED BY MG2+ AND CA2+.  
CC    -!- SUBUNIT: MONOMER.  
CC    -!- SUBCELLULAR LOCATION: SECRETED.  
DR    GO; GO:0016787; F:hydrolase activity; IEA.  
DR    GO; GO:0008237; F:metallopeptidase activity; IEA.  
KW    Hydrolase; Metalloprotease.  
FT    NON\_TER           14        14  
SQ    SEQUENCE    14 AA;    1373 MW;    14D627940C973260 CRC64;

Query Match                    52.4%;    Score 22;    DB 2;    Length 14;  
Best Local Similarity    60.0%;    Pred. No. 1.9e+03;  
Matches        3;    Conservative    1;    Mismatches    1;    Indels        0;    Gaps        0;

Qy            3 PPPLP 7  
             || :|  
Db            4 PPDIP 8

RESULT 9

Q9TRR1

ID    Q9TRR1            PRELIMINARY;            PRT;        16 AA.  
AC    Q9TRR1;  
DT    01-MAY-2000 (TrEMBLrel. 13, Created)  
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT    01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Fibronectin 47 kDa fragment (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92283375; PubMed=1597256;  
 RA Lesot H., Fausser J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,  
 RA Ruch J.V.;  
 RT "The carboxy-terminal extension of the collagen binding domain of  
 RT fibronectin mediates interaction with a 165 kDa membrane protein  
 RT involved in odontoblast differentiation."  
 RL Differentiation 49:109-118(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1764 MW; B196CAAAC53F5739 CRC64;

Query Match 52.4%; Score 22; DB 6; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 || ||  
 Db 1 QPQPHP 6

#### RESULT 10

Q90XE2

ID Q90XE2 PRELIMINARY; PRT; 17 AA.  
 AC Q90XE2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Transforming growth factor beta 4 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pan H.J., Halper J.;  
 RT "5' end sequence of chicken transforming growth factor beta 4."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF395834; AAL05481.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1721 MW; 5080B3551E71BD63 CRC64;

Query Match 52.4%; Score 22; DB 13; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
 || ||  
 Db 1 MDPSPPL 6

RESULT 11

Q9Q0W9

ID Q9Q0W9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0W9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UMEA3;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119350; AAF24106.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
 |||  
 Db 7 PPP 9

RESULT 12

Q8JV70

ID Q8JV70 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV70;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USA 5;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA.";  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304387; AAM97804.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 13

Q9Q0W1

ID Q9Q0W1 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CSFB;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage."  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119354; AAF24114.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 14

Q8JV68

ID Q8JV68 PRELIMINARY; PRT; 10 AA.  
AC Q8JV68;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USA 6;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA.";  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF304388; AAM97806.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
| | |  
Db 7 PPP 9

RESULT 15

Q9Q0V9

ID Q9Q0V9 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0V9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CSFE;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119355; AAF24116.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
| | |  
Db 7 PPP 9

RESULT 16

Q9Q0W7

ID Q9Q0W7 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).



OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NANCY2;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119351; AAF24108.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 7 PPP 9

#### RESULT 17

Q8JV66

ID Q8JV66 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV66;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSF K;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF304389; AAM97808.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 7 PPP 9

RESULT 18

Q9Q0V7

ID Q9Q0V7 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0V7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CSFJ;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119356; AAF24118.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 7 PPP 9

RESULT 19

Q8JV82

ID Q8JV82 PRELIMINARY; PRT; 10 AA.  
 AC Q8JV82;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E1;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303944; AAM97792.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 20

Q8JV76

ID Q8JV76 PRELIMINARY; PRT; 10 AA.  
AC Q8JV76;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USA2;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA.";  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303947; AAM97798.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 21

Q8JV74

ID Q8JV74 PRELIMINARY; PRT; 10 AA.  
AC Q8JV74;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USA3;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA.";  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303948; AAM97800.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 22

Q9Q0W5

ID Q9Q0W5 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PRETORIA3;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage.";  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119352; AAF24110.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 23

Q9Q0X3

ID Q9Q0X3 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0X3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).

OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCN8;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119348; AAF24102.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 7 PPP 9

#### RESULT 24

Q9Q0X5

ID Q9Q0X5 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0X5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCN16;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119347; AAF24100.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 7 PPP 9

#### RESULT 25

Q9Q0W3

ID Q9Q0W3 PRELIMINARY; PRT; 10 AA.  
AC Q9Q0W3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PRETORIAL;  
RX MEDLINE=20087544; PubMed=10618230;  
RA Bofill-Mas S., Pina S., Girones R.;  
RT "Documenting the epidemiologic patterns of polyomaviruses in human  
RT populations by studying their presence in urban sewage."  
RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119353; AAF24112.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

RESULT 26

Q8JV80

ID Q8JV80 PRELIMINARY; PRT; 10 AA.  
AC Q8JV80;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E2;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF303945; AAM97794.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||

Db 7 PPP 9

RESULT 27

Q9Q0X1

ID Q9Q0X1 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0X1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCN15;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage."  
 RL Appl. Environ. Microbiol. 66:238-245(2000).  
 DR EMBL; AF119349; AAF24104.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||

Db 7 PPP 9

RESULT 28

Q9Q0X9

ID Q9Q0X9 PRELIMINARY; PRT; 10 AA.  
 AC Q9Q0X9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCNU;  
 RX MEDLINE=20087544; PubMed=10618230;  
 RA Bofill-Mas S., Pina S., Girones R.;  
 RT "Documenting the epidemiologic patterns of polyomaviruses in human  
 RT populations by studying their presence in urban sewage.";

RL Appl. Environ. Microbiol. 66:238-245(2000).  
DR EMBL; AF119345; AAF24096.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

#### RESULT 29

Q8JV72

ID Q8JV72 PRELIMINARY; PRT; 10 AA.  
AC Q8JV72;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Large T antigen (Fragment).  
OS Polyomavirus JC.  
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
OX NCBI\_TaxID=10632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USA 4;  
RX MEDLINE=21465052; PubMed=11581397;  
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
RA Girones R.;  
RT "Potential transmission of human polyomaviruses through the  
RT gastrointestinal tract after exposure to virions or viral DNA."  
RL J. Virol. 75:10290-10299(2001).  
DR EMBL; AF304386; AAM97802.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 50.0%; Score 21; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

#### RESULT 30

P82436

ID P82436 PRELIMINARY; PRT; 11 AA.  
AC P82436;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE 65 kDa cell wall protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

Query Match 50.0%; Score 21; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 2 PPP 4

#### RESULT 31

##### Q8UUP1

ID Q8UUP1 PRELIMINARY; PRT; 11 AA.  
 AC Q8UUP1;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Beta-TrCP protein (Fragment).  
 GN BETA-TRCP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carnevali F.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ballarino M.;  
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus  
 RT laevis.";  
 RL Thesis (2001), Department of Genetica e Biologia Molecolare,  
 RL University of Rome La Sapienza, Rome, Italy.  
 DR EMBL; AJ428930; CAD21927.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 50.0%; Score 21; DB 13; Length 11;

Best Local Similarity 75.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPP 4  
:|||  
Db 8 LQPP 11

RESULT 32

Q9BZ49

ID Q9BZ49 PRELIMINARY; PRT; 12 AA.  
AC Q9BZ49;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Glycophorin C (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
RA Zimmerman P.A.;  
RT "The association of the glycophorin C exon 3 deletion with  
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
RT Guinea.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF342984; AAK01459.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 50.0%; Score 21; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 9 PPP 11

RESULT 33

Q93X21

ID Q93X21 PRELIMINARY; PRT; 12 AA.  
AC Q93X21;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Polyubiquitin homolog (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=cv. INRA 258; TISSUE=Leaf;  
RX MEDLINE=96236829; PubMed=8680303;  
RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;  
RT "Heavy-metal-responsive genes in maize: identification and comparison  
RT of their expression upon various forms of abiotic stress."  
RL Planta 199:1-8(1996).  
DR EMBL; S82313; AAB47175.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 50.0%; Score 21; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
| | |  
Db 2 PPP 4

#### RESULT 34

Q9UCC2

ID Q9UCC2 PRELIMINARY; PRT; 15 AA.  
AC Q9UCC2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 35 kDa heparin-RELEASABLE protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94059921; PubMed=8241100;  
RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;  
RT "Identification of novel heparin-releasable proteins, as well as the  
RT cytokines midkine and pleiotrophin, in human postheparin plasma."  
RL Arterioscler. Thromb. 13:1798-1805(1993).  
SQ SEQUENCE 15 AA; 1454 MW; 0585FEF4FE8F6265 CRC64;

Query Match 50.0%; Score 21; DB 4; Length 15;  
Best Local Similarity 60.0%; Pred. No. 3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPLP 7  
| | : |  
Db 5 PVPIP 9

#### RESULT 35

Q9TR14

ID Q9TR14 PRELIMINARY; PRT; 15 AA.  
AC Q9TR14;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide

DE (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96187584; PubMed=8611748;  
 RA Nakai Y., Nishimura T., Shimizu M., Arai S.;  
 RT "Effects of freezing on the proteolysis of beef during storage at 4  
 RT degrees C.";  
 RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).  
 SQ SEQUENCE 15 AA; 1597 MW; C98A5B44A79E4777 CRC64;

Query Match 50.0%; Score 21; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 2 PPP 4

#### RESULT 36

Q9S8N8

ID Q9S8N8 PRELIMINARY; PRT; 15 AA.  
 AC Q9S8N8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Protein E-22 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94170739; PubMed=8125056;  
 RA Flengsrud R.;  
 RT "Separation of acidic barley endosperm proteins by two-dimensional  
 RT electrophoresis.";  
 RL Electrophoresis 14:1060-1066(1993).  
 SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 50.0%; Score 21; DB 10; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPP 4  
 :|||  
 Db 3 LQPP 6

#### RESULT 37

Q14001

ID Q14001 PRELIMINARY; PRT; 17 AA.  
AC Q14001;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Cyclic nucleotide phosphodiesterase (Fragment).  
GN CGIPDE1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97079687; PubMed=8921398;  
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;  
RT "Molecular cloning and chromosomal assignment of the human homologue  
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved  
RT in fat metabolism located at 11p15.1."  
RL Genomics 37:211-218(1996).  
DR EMBL; X95522; CAA64776.1; -.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 50.0%; Score 21; DB 4; Length 17;  
Best Local Similarity 75.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPP 4  
:| | |  
Db 14 LQPP 17

# RESULT 38

## Q9TR22

ID Q9TR22 PRELIMINARY; PRT; 17 AA.  
AC Q9TR22;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE NONAMELOGENIN glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96126798; PubMed=8564801;  
RA Punzi J.S., DenBesten P.K.;  
RT "Purification of nonamelogenin proteins from bovine secretory  
RT enamel."  
RL Calcif. Tissue Int. 57:379-384(1995).  
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 50.0%; Score 21; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 8 PPP 10

RESULT 39

O49225

ID O49225 PRELIMINARY; PRT; 17 AA.  
AC O49225;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hydroxyproline-rich glycoprotein (Fragment).  
GN HRGP.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RX MEDLINE=94211912; PubMed=8159793;  
RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;  
RT "Isolation and characterization of three soybean extensin cDNAs."  
RL Plant Physiol. 104:793-796(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Essex; TISSUE=Root;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF047052; AAC03558.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 50.0%; Score 21; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 11 PPP 13

RESULT 40

Q8NFB4

ID Q8NFB4 PRELIMINARY; PRT; 18 AA.  
AC Q8NFB4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Mutant enamelin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kida M., Ariga T.;  
 RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused  
 RT by an enamelin gene mutation at exon-intron boundary."  
 RL J. Dent. Res. 0:0-0(2002).  
 DR EMBL; AF530444; AAM97323.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3E8BE512 CRC64;

Query Match 50.0%; Score 21; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
 |||  
 Db 3 PPP 5

#### RESULT 41

Q9H1I3

ID Q9H1I3 PRELIMINARY; PRT; 18 AA.  
 AC Q9H1I3;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Retinoic acid receptor gamma (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Xu H., Clifford J.L.;  
 RT "Genomic organization of the human retinoic acid receptor gamma  
 RT gene."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY013704; AAG41595.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1964 MW; A284A1EFBB361A22 CRC64;

Query Match 50.0%; Score 21; DB 4; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 | | : |  
 Db 12 PGPM 16

#### RESULT 42

Q9JIE9

ID Q9JIE9 PRELIMINARY; PRT; 18 AA.

AC Q9JIE9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Protein arginine N-methyltransferase 1 (Fragment).  
 GN MRMT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20307889; PubMed=10848611;  
 RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;  
 RT "Arginine N-methyltransferase 1 is required for early postimplantation  
 RT mouse development, but cells deficient in the enzyme are viable.";  
 RL Mol. Cell. Biol. 20:4859-4869(2000).  
 DR EMBL; AF232718; AAF37294.1; -.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Methyltransferase; Transferase.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1931 MW; 392E2C312C4A8372 CRC64;

Query Match 50.0%; Score 21; DB 11; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQPP 4  
 :|||  
 Db 12 LQPP 15

#### RESULT 43

##### Q8QFT3

ID Q8QFT3 PRELIMINARY; PRT; 18 AA.  
 AC Q8QFT3;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Sterol regulatory element binding protein 1 (Fragment).  
 GN SREBP-1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Assaf S., Pitel F., Morisson M., Alizadeh M., Gondret F., Diot C.,  
 RA Leclercq B., Vignal A., Douaire M., Lagarrigue S.;  
 RT "Partial cloning, tissue expression, chromosomal localisation of  
 RT chicken SREBP genes and relationships to fatness variability in  
 RT genetically fat and lean chicken lines.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ441122; CAD29619.1; -.



FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 1947 MW; 3206A67750EFD7EA CRC64;

Query Match 50.0%; Score 21; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 15 PPP 17

#### RESULT 44

##### Q9UCS8

ID Q9UCS8 PRELIMINARY; PRT; 9 AA.  
AC Q9UCS8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Apolipoprotein A-I (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92075698; PubMed=1742316;  
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirszbaum L., Metso J.,  
RA Murphy B., Walker I.D.;  
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40  
RT protein of human blood are different proteins which both bind to  
RT apolipoprotein A-I.";  
RL Biochim. Biophys. Acta 1086:255-260(1991).  
DR GO; GO:0005576; C:extracellular; ISS.  
DR GO; GO:0005319; F:lipid transporter activity; NAS.  
DR GO; GO:0008203; P:cholesterol metabolism; ISS.  
DR GO; GO:0006869; P:lipid transport; ISS.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 47.6%; Score 20; DB 4; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1e+06;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:|| |  
Db 2 EPPQSP 7

#### RESULT 45

##### Q8IVG8

ID Q8IVG8 PRELIMINARY; PRT; 11 AA.  
AC Q8IVG8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Low density lipoprotein receptor related protein 1 (Fragment).  
 GN LRP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Schulz S., Schagdarsurengin U., Greiser P., Birkenmeier G.,  
 RA Muller-Werdan U., Hagemann M., Riemann D., Werdan K., Glaser C.;  
 RT "The LDL receptor-related protein (LRP1/A2MR) and coronary  
 RT atherosclerosis - novel genomic variants and functional  
 RT consequences.";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; Y18524; CAD57169.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor; Lipoprotein.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1221 MW; 373D041E27273777 CRC64;

Query Match 47.6%; Score 20; DB 4; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPL 6  
 | |||  
 Db 1 MLTPPL 6

#### RESULT 46

P82441

ID P82441 PRELIMINARY; PRT; 12 AA.  
 AC P82441;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 26 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON\_TER 12 12

SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

Query Match 47.6%; Score 20; DB 10; Length 12;  
Best Local Similarity 75.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 2 PPAP 5

RESULT 47

Q67604

ID Q67604 PRELIMINARY; PRT; 13 AA.  
AC Q67604;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Movement protein (Fragment).  
GN BC1.  
OS Squash leaf curl virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10829;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Los Mochis 1;  
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;  
RT "Diversity among geminiviruses associated with vegetables from Valle  
RT del Fuerte, Sinaloa, Mexico."  
RL Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; L27273; AAA47820.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1376 MW; D471DE4D634E76C2 CRC64;

Query Match 47.6%; Score 20; DB 12; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQPP 4  
:|||  
Db 6 VQPP 9

RESULT 48

Q9UQS4

ID Q9UQS4 PRELIMINARY; PRT; 16 AA.  
AC Q9UQS4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Glycoprotein Ib alpha variant D (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92250564; PubMed=1577776;  
 RA Lopez J.A., Ludwig E.H., McCarthy B.J.;  
 RT "Polymorphism of human glycoprotein Ib alpha results from a variable  
 RT number of tandem repeats of a 13-amino acid sequence in the mucin-like  
 RT macroglycopeptide region. Structure/function implications.";  
 RL J. Biol. Chem. 267:10055-10061(1992).  
 DR EMBL; S34436; AAB22152.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 16 AA; 1638 MW; 81472B42262EF630 CRC64;

Query Match 47.6%; Score 20; DB 4; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 :| | |  
 Db 5 EPAPSP 10

#### RESULT 49

Q8RVF4

ID Q8RVF4 PRELIMINARY; PRT; 16 AA.  
 AC Q8RVF4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Proline rich protein (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. H98, and cv. C123;  
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,  
 RA Morgante M., Rafalski J.A.;  
 RT "SNP frequency, haplotype structure and linkage disequilibrium in  
 RT elite maize inbred lines.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY094252; AAM15707.1; -.  
 DR EMBL; AY094253; AAM15708.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 16 AA; 1720 MW; 02F6CD77295E5610 CRC64;

Query Match 47.6%; Score 20; DB 10; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPPL 6  
 | | |  
 Db 10 QCPPL 14

#### RESULT 50

Q96P96

ID Q96P96 PRELIMINARY; PRT; 17 AA.  
 AC Q96P96;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NHP2-like protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;  
 RT "Characterization of TPA-responsive genes in U937 cells using ordered  
 RT differential display PCR."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF401217; AAL02173.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 47.6%; Score 20; DB 4; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 5e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 :| |||  
 Db 10 VQSLPLP 16

Search completed: July 4, 2004, 04:45:22  
 Job time : 16.9104 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 2.40299 Seconds  
 (without alignments)  
 151.683 Million cell updates/sec

Title: US-09-641-802-1  
 Perfect score: 42  
 Sequence: 1 MQPPPLP 7

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7  
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26	61.9	17	1	APID_BOMPA	P81464 bombus pasc
2	25	59.5	10	1	TMOF_AEDAE	P19425 aedes aegyp
3	23	54.8	11	1	BPP_AGKHP	P04562 agkistrodon
4	23	54.8	13	1	TY13_PHYRO	P04096 phyllomedus
5	22	52.4	15	1	URE2_MORMO	P17338 morganella
6	22	52.4	17	1	A45K_MYCBO	P80069 mycobacteri
7	21	50.0	15	1	PRP_MYCBO	P80149 mycobacteri
8	21	50.0	15	1	UC29_MAIZE	P80635 zea mays (m
9	21	50.0	16	1	IBP4_PIG	P24854 sus scrofa
10	20	47.6	16	1	FOR2_MYRGU	P81437 myrmecia gu
11	19	45.2	11	1	BPP3_BOTIN	P30423 bothrops in
12	19	45.2	11	1	BPP4_BOTIN	P30424 bothrops in
13	19	45.2	11	1	BPPB_AGKHA	P01021 agkistrodon
14	19	45.2	11	1	MORN_HUMAN	P01163 homo sapien
15	19	45.2	12	1	FIF1_SARBU	P83349 sarcophaga
16	19	45.2	17	1	PSBL_SYNVU	P12241 synechococc
17	18	42.9	9	1	YBFR_AZOVI	P25825 azotobacter

18	18	42.9	11	1	TIN4_HOPTI	P82654	hoplobatr
19	18	42.9	11	1	TKN1_UPERU	P08612	uperoleia r
20	18	42.9	12	1	TIN2_HOPTI	P82652	hoplobatr
21	18	42.9	12	1	TIN3_HOPTI	P82653	hoplobatr
22	18	42.9	13	1	PEDI_HYDAT	P80578	hydra atten
23	18	42.9	14	1	ECDC_LYMDI	P80940	lymantria d
24	18	42.9	15	1	AF1L_MALPA	P83141	malva parvi
25	18	42.9	15	1	MK1_PALPR	P80408	palomena pr
26	18	42.9	15	1	MK2A_PALPR	P80409	palomena pr
27	18	42.9	16	1	FOR1_MYRGU	P81438	myrmecia gu
28	18	42.9	16	1	MK2B_PALPR	P80410	palomena pr
29	18	42.9	16	1	MK3_PALPR	P80411	palomena pr
30	17	40.5	10	1	BPP8_BOTIN	P30426	bothrops in
31	17	40.5	11	1	LADD_ONCMY	P81018	oncorhynch
32	17	40.5	11	1	TKN1_PSEGU	P42986	pseudophryn
33	17	40.5	11	1	TKN2_PSEGU	P42987	pseudophryn
34	17	40.5	11	1	TKN3_PSEGU	P42988	pseudophryn
35	17	40.5	11	1	TKN4_PSEGU	P42989	pseudophryn
36	17	40.5	11	1	TKN5_PSEGU	P42990	pseudophryn
37	17	40.5	12	1	TKN2_KASMA	P08614	kassina mac
38	17	40.5	13	1	GER1_HORVU	P28525	hordeum vul
39	17	40.5	13	1	GER2_HORVU	P28526	hordeum vul
40	17	40.5	13	1	SODM_CANFA	P54712	canis famil
41	17	40.5	15	1	SODM_ENTAE	P22799	enterobacte
42	16	38.1	8	1	PPK2_PERAM	P82692	periplaneta
43	16	38.1	9	1	FAR9_ASCSU	P43172	ascaris suu
44	16	38.1	9	1	MGMT_BOVIN	P29177	bos taurus
45	16	38.1	10	1	AH3_PRUSE	P29261	prunus sero
46	16	38.1	10	1	BPP2_BOTIN	P30422	bothrops in
47	16	38.1	10	1	BPP2_BOTJA	P01022	bothrops ja
48	16	38.1	10	1	UPA2_HUMAN	P30088	homo sapien
49	16	38.1	11	1	TIN1_HOPTI	P82651	hoplobatr
50	16	38.1	12	1	TM2A_METMA	P80652	methanosarc
51	16	38.1	13	1	AH4_PRUSE	P29262	prunus sero
52	16	38.1	15	1	AH2_PRUSE	P29260	prunus sero
53	16	38.1	15	1	NUO8_SOLTU	P80731	solanum tub
54	16	38.1	15	1	SODM_STRGR	P80733	streptomyce
55	16	38.1	16	1	AH1_PRUSE	P29259	prunus sero
56	15	35.7	7	1	TPFY_PACDA	P83455	pachymedusa
57	15	35.7	7	1	UF04_MOUSE	P38642	mus musculu
58	15	35.7	9	1	COXE_THUOB	P80975	thunnus obe
59	15	35.7	9	1	KNL3_BOMVA	P83058	bombina var
60	15	35.7	9	1	LMT3_LOCFI	P41489	locusta mig
61	15	35.7	10	1	BRK_ONCMY	Q9prz1	oncorhynch
62	15	35.7	10	1	URE3_MORMO	P17339	morganella
63	15	35.7	11	1	BRK_MEGFL	P12797	megascolia
64	15	35.7	12	1	FAR7_PENMO	P83322	penaeus mon
65	15	35.7	12	1	TKN1_KASMA	P08613	kassina mac
66	15	35.7	13	1	BLAC_STRGR	P81173	streptomyce
67	15	35.7	13	1	BPP1_BOTJA	P01020	bothrops ja
68	15	35.7	13	1	BRK_PARID	P42717	parapolybia
69	15	35.7	13	1	MP1_MICOC	P81532	microplitis
70	15	35.7	14	1	CAL1_CALGI	P20728	calotropis
71	15	35.7	14	1	PH1_PRUSE	P29263	prunus sero
72	15	35.7	15	1	CBPB_PROAT	P19628	protopterus
73	15	35.7	15	1	PH3_PRUSE	P29265	prunus sero
74	15	35.7	15	1	UBL1_MONDO	P50103	monodelphis

75	15	35.7	15	1	UC19_MAIZE	P80625	zea mays (m
76	15	35.7	15	1	UC30_MAIZE	P80636	zea mays (m
77	15	35.7	15	1	UP01_METAN	P83440	metarhizium
78	15	35.7	16	1	H5_COTJA	P18638	coturnix co
79	15	35.7	16	1	LPK1_LOCFI	P20404	locusta mig
80	15	35.7	16	1	PH2_PRUSE	P29264	prunus sero
81	15	35.7	17	1	VESP_VESMC	P57672	vespula mac
82	14	33.3	8	1	ALL5_CALVO	P41841	calliphora
83	14	33.3	8	1	VGLG_HSV2B	P81780	herpes simp
84	14	33.3	10	1	BPP_VIPAS	P31351	vipera aspi
85	14	33.3	10	1	GON1_ALLMI	P37041	alligator m
86	14	33.3	10	1	RT02_BOVIN	P82923	bos taurus
87	14	33.3	10	1	UPA5_HUMAN	P30091	homo sapien
88	14	33.3	10	1	UPA8_HUMAN	P30094	homo sapien
89	14	33.3	11	1	TKNA_HORSE	P01290	equus cabal
90	14	33.3	11	1	TKNA_RANCA	P22688	rana catesb
91	14	33.3	13	1	EI21_LITRU	P82097	litoria rub
92	14	33.3	13	1	EI22_LITRU	P82098	litoria rub
93	14	33.3	15	1	CHI1_PEA	P21225	pisum sativ
94	14	33.3	15	1	CXA2_CONAL	P56640	conus aulic
95	14	33.3	15	1	UC06_MAIZE	P80612	zea mays (m
96	14	33.3	15	1	UE15_HORVU	P34938	hordeum vul
97	14	33.3	15	1	UP02_METAN	P83439	metarhizium
98	14	33.3	16	1	AF1S_MALPA	P83140	malva parvi
99	14	33.3	16	1	AF2S_MALPA	P83142	malva parvi
100	14	33.3	16	1	CXA1_CONAL	P56639	conus aulic

#### ALIGNMENTS

##### RESULT 1

APID\_BOMPA

ID APID\_BOMPA STANDARD; PRT; 17 AA.

AC P81464;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Apidaecin.

OS Bombus pascuorum (Brown bumble bee).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

OC Apidae; Bombus.

OX NCBI\_TaxID=65598;

RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RX MEDLINE=97362903; PubMed=9219367;

RA Rees J.A., Moniatte M., Bulet P.;

RT "Novel antibacterial peptides isolated from a European bumblebee,

RT Bombus pascuorum (Hymenoptera, Apoidea).";

RL Insect Biochem. Mol. Biol. 27:413-422(1997).

CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
bacteria.

CC -!- INDUCTION: By bacterial infection.

DR InterPro; IPR004828; Apidaecin.

DR Pfam; PF00807; Apidaecin; 1.



KW Insect immunity; Antibiotic; Hemolymph.

SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64; .

Query Match 61.9%; Score 26; DB 1; Length 17;

Best Local Similarity 80.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7

||| |

Db 8 PPPRP 12

## RESULT 2

### TMOF\_AEDAE

ID TMOF\_AEDAE STANDARD; PRT; 10 AA.

AC P19425;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Trypsin-modulating oostatic factor (TMOF) (OOSH).

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

OX NCBI\_TaxID=7159;

RN [1]

RP SEQUENCE.

RC STRAIN=Vero beach; TISSUE=Ovary;

RX MEDLINE=90367888; PubMed=2394318;

RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;

RT "Mosquito oostatic factor: a novel decapeptide modulating

RT trypsin-like enzyme biosynthesis in the midgut.";

RL FASEB J. 4:3015-3020(1990).

RN [2]

RP SEQUENCE.

RC STRAIN=Vero beach; TISSUE=Ovary;

RX MEDLINE=93357794; PubMed=8353526;

RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;

RT "Mass spectrometry and characterization of Aedes aegypti trypsin

RT modulating oostatic factor (TMOF) and its analogs.";

RL Insect Biochem. Mol. Biol. 23:703-712(1993).

CC -!- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis

CC in the midgut which indirectly reduces the vitellogenin

CC concentration in the hemolymph resulting in inhibition of oocyte

CC development.

CC -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular

CC epithelium 18-24 hrs after a blood meal. Synthesis peaks at

CC 36 hrs and stops at 56 hrs.

DR PIR; A36454; A36454.

KW Hormone.

FT DOMAIN 3 10 POLY-PRO.

FT VARIANT 1 2 YD -> DY (IN TMFO(B)).

SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 59.5%; Score 25; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
| | | |  
Db 5 P P P P P 9

RESULT 3

BPP\_AGKHP

ID BPP\_AGKHP STANDARD; PRT; 11 AA.  
AC P04562;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys  
OS pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=86177022; PubMed=3008123;  
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RT "Structure-function studies on the bradykinin potentiating peptide  
RT from Chinese snake venom (Agkistrodon halys pallas).";  
RL Peptides 6 Suppl. 3:339-342(1985).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; JC0002; XAVIBH.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
| | : |  
Db 7 PPIP 10

RESULT 4

TY13\_PHYRO

ID TY13\_PHYRO STANDARD; PRT; 13 AA.  
AC P04096;  
DT 01-NOV-1986 (Rel. 03, Created)  
DT 01-NOV-1986 (Rel. 03, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-13.  
OS Phyllomedusa rohdei (Rohde's leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Phyllomedusinae; Phyllomedusa.  
 OX NCBI\_TaxID=8394;  
 RN [1]  
 RP SEQUENCE.  
 RA Montecucchi P.C., Gozzini L., Erspamer V.;  
 RT "Primary structure determination of a tryptophan-containing  
 RT tridecapeptide from Phyllomedusa rohdei."  
 RL Int. J. Pept. Protein Res. 27:175-182(1986).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR PIR; A05174; A05174.  
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 54.8%; Score 23; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPL 6  
 |||:  
 Db 7 PPPI 10

#### RESULT 5

##### URE2\_MORMO

ID URE2\_MORMO STANDARD; PRT; 15 AA.  
 AC P17338;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea  
 DE amidohydrolase) (Fragment).  
 GN UREB.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences."  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- SUBUNIT: (Alpha, beta, gamma)(3) (By similarity).  
 CC -!- SIMILARITY: Belongs to the urease beta subunit family.  
 DR PIR; B35389; B35389.  
 KW Hydrolase.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPPL 6  
|| ||  
Db 5 QPTPL 9

RESULT 6

A45K\_MYCBO

ID A45K\_MYCBO STANDARD; PRT; 17 AA.  
AC P80069;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE 45/47 kDa antigen (Fragment).  
OS Mycobacterium bovis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=BCG / Paris 1173 P2;  
RX MEDLINE=93138802; PubMed=8423100;  
RA Romain F., Laqueyrie A., Militzer P., Pescher P., Chavarot P.,  
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;  
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen  
RT complex, an immunodominant target for antibody response after  
RT immunization with living bacteria.";  
RL Infect. Immun. 61:742-750(1993).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.  
DR PIR; A49237; A49237.  
KW Antigen.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 52.4%; Score 22; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 4.8e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPLP 7  
||:|  
Db 6 PPVP 9

RESULT 7

PRP\_MYCBO

ID PRP\_MYCBO STANDARD; PRT; 15 AA.  
AC P80149;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Proline-rich protein (Fragment).  
OS Mycobacterium bovis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1765;  
RN [1]  
RP SEQUENCE.

RC STRAIN=BCG / Paris 1173 P2;  
RX MEDLINE=93281750; PubMed=8506381;  
RA Romain F., Augier J., Pescher P., Marchal G.A.;  
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-  
RT type hypersensitivity reactions only in guinea pigs immunized with  
RT living mycobacteria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY  
CC REACTIONS IN GUINEA PIGS.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 50.0%; Score 21; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5  
|||  
Db 7 PPP 9

#### RESULT 8

##### UC29\_MAIZE

ID UC29\_MAIZE STANDARD; PRT; 15 AA.  
AC P80635;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.9, its MW is: 37.6 kDa.  
DR Maize-2DPAGE; P80635; COLEOPTILE.  
DR MaizeDB; 123960; -.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 50.0%; Score 21; DB 1; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPLP 7

Db                    | | : |  
                      4 PVPIP 8

RESULT 9

IBP4\_PIG

ID    IBP4\_PIG                    STANDARD;            PRT;        16 AA.  
AC    P24854;  
DT    01-MAR-1992 (Rel. 21, Created)  
DT    01-MAR-1992 (Rel. 21, Last sequence update)  
DT    28-FEB-2003 (Rel. 41, Last annotation update)  
DE    Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)  
DE    (IGF-binding protein 4) (Fragment).  
GN    IGFBP4.  
OS    Sus scrofa (Pig).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX    NCBI\_TaxID=9823;  
RN    [1]  
RP    SEQUENCE.  
RX    MEDLINE=92109718; PubMed=1722398;  
RA    Coleman M.E., Pan Y.-C.E., Etherton T.D.;  
RT    "Identification and NH2-terminal amino acid sequence of three  
RT    insulin-like growth factor-binding proteins in porcine serum."  
RL    Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
CC    -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs  
CC        and have been shown to either inhibit or stimulate the growth  
CC        promoting effects of the IGFs on cell culture. They alter the  
CC        interaction of IGFs with their cell surface receptors.  
CC    -!- SUBCELLULAR LOCATION: Secreted.  
CC    -!- SIMILARITY: Contains 1 IGFBP domain.  
CC    -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
DR    PIR; JH0517; JH0517.  
DR    InterPro; IPR000867; Insl\_gro\_fac\_pr.  
DR    InterPro; IPR000716; Thyroglobulin\_1.  
DR    PROSITE; PS00222; IGF\_BINDING; PARTIAL.  
DR    PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
KW    Growth factor binding.  
FT    NON\_TER            16        16  
SQ    SEQUENCE    16 AA;    1799 MW;    40988840096655E2 CRC64;

Query Match                    50.0%;    Score 21;    DB 1;    Length 16;  
Best Local Similarity    100.0%;    Pred. No. 6.3e+02;  
Matches        3;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    3 PPP 5  
                      | | |  
Db                    7 PPP 9

RESULT 10

FOR2\_MYRGU

ID    FOR2\_MYRGU                    STANDARD;            PRT;        16 AA.  
AC    P81437;  
DT    15-DEC-1998 (Rel. 37, Created)  
DT    15-DEC-1998 (Rel. 37, Last sequence update)  
DT    10-OCT-2003 (Rel. 42, Last annotation update)

DE Formaecin 2.  
 OS Myrmecia gulosa (Red bulldog ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.  
 OX NCBI\_TaxID=36170;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=98165787; PubMed=9497332;  
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
 RT "Isolation from an ant Myrmecia gulosa of two inducible  
 RT O-glycosylated proline-rich antibacterial peptides.";  
 RL J. Biol. Chem. 273:6139-6143(1998).  
 CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli but  
 CC none against other Gram-negative bacteria and Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- INDUCTION: By bacterial infection.  
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.  
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 47.6%; Score 20; DB 1; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 8.8e+02;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
 :| | |  
 Db 9 KPTYPY 14

# RESULT 11

## BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
 AC P30423;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; C37196; C37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 4 PPRP 7

#### RESULT 12

##### BPP4\_BOTIN

ID BPP4\_BOTIN STANDARD; PRT; 11 AA.  
AC P30424;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom."  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; D37196; D37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 4 PPRP 7



# RESULT 13

## BPPB\_AGKHA

ID BPPB\_AGKHA STANDARD; PRT; 11 AA.  
AC P01021;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide B (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=242054;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Kato H., Suzuki T.;  
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from  
RT the venom of Agkistrodon halys blomhoffii.";  
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01254; XASNBA.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
|||  
Db 4 PPRP 7

# RESULT 14

## MORN\_HUMAN

ID MORN\_HUMAN STANDARD; PRT; 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human),  
OS Rattus norvegicus (Rat),  
OS Bos taurus (Bovine),  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]

RP SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RX MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
RT from coelenterates to humans.";  
RL Nature 293:579-580(1981).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=A.elegantissima, and H.attenuata;  
RA Schaller H.C., Bodenmuller H.;  
RT "Isolation and amino acid sequence of a morphogenetic peptide from  
RT hydra.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
RN [3]  
RP SYNTHESIS.  
RX MEDLINE=82050803; PubMed=7297679;  
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
RT "Synthesis of a new neuropeptide, the head activator from hydra.";  
RL FEBS Lett. 131:317-321(1981).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=90059923; PubMed=2583101;  
RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
RT in the G2/mitosis transition.";  
RL EMBO J. 8:3311-3318(1989).  
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells  
CC in the G2/mitosis transition.  
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra  
CC and was called head activator by the authors, because it induced  
CC head-specific growth and differentiation in this animal. It has  
CC been found in mammalian intestine and hypothalamus.  
DR PIR; A01427; YHRT.  
DR PIR; A93900; YHXAE.  
DR PIR; B01427; YHHU.  
DR PIR; B93900; YHJFHY.  
DR PIR; C01427; YHBO.  
DR GK; P01163; -.  
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPP 4  
| | |  
Db 1 QPP 3

RESULT 15  
FIF1\_SARBU  
ID FIF1\_SARBU STANDARD; PRT; 12 AA.  
AC P83349;  
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neb-FIRFamide 1.  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AMIDATION, AND FUNCTION.  
 RC TISSUE=CNS;  
 RX MEDLINE=22342733; PubMed=12438685;  
 RA Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
 RT "Identification in Drosophila melanogaster of the invertebrate G  
 RT protein-coupled FMRFamide receptor."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
 CC junctions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 9.1e+02;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPLP 7  
 |||  
 Db 2 PPQP 5

#### RESULT 16

##### PSBL\_SYNVU

ID PSBL\_SYNVU STANDARD; PRT; 17 AA.  
 AC P12241;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Photosystem II reaction center L protein (PSII 5 kDa protein)  
 DE (Fragment).  
 GN PSBL.  
 OS Synechococcus vulcanus (Thermosynechococcus vulcanus).  
 OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.  
 OX NCBI\_TaxID=32053;  
 RN [1]  
 RP SEQUENCE.  
 RA Ikeuchi M., Koike H., Inoue Y.;  
 RT "Identification of psbI and psbL gene products in cyanobacterial  
 RT photosystem II reaction center preparation."  
 RL FEBS Lett. 251:155-160(1989).  
 CC -!- FUNCTION: Not known, it is however required for PSII activity.  
 CC -!- SUBCELLULAR LOCATION: Cellular thylakoid membrane.  
 CC -!- SIMILARITY: Belongs to the psbL family.

DR PIR; S05033; S05033.  
DR HAMAP; MF\_01317; -; 1.  
DR InterPro; IPR003372; PSII\_PsbL.  
DR Pfam; PF02419; PsbL; 1.  
KW Photosynthesis; Thylakoid; Photosystem II; Reaction center.  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match 45.2%; Score 19; DB 1; Length 17;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPPP 5  
|:| |  
Db 1 MEPNP 5

RESULT 17

YBFR\_AZOVI

ID YBFR\_AZOVI STANDARD; PRT; 9 AA.  
AC P25825;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in bfr 3'region (Fragment).  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92196129; PubMed=1549605;  
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,  
RA Stiefel E.I.;  
RT "Unification of the ferritin family of proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).

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DR EMBL; M83692; AAA22122.1; -.  
DR PIR; B41983; B41983.  
KW Hypothetical protein.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 42.9%; Score 18; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPP 4  
| ||

RESULT 18

TIN4\_HOPTI

ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
 AC P82654;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tigerinin-4.  
 OS *Hoplobatrachus tigerinus* (Indian bull frog) (*Rana tigerina*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
 OC *Hoplobatrachus*.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*  
 RT *tigerina*."  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,  
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 42.9%; Score 18; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7  
 |||  
 Db 7 PLP 9

RESULT 19

TKN1\_UPERU

ID TKN1\_UPERU STANDARD; PRT; 11 AA.  
 AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS *Uperoleia rugosa* (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC *Myobatrachinae*; *Uperoleia*.  
 OX NCBI\_TaxID=8368;  
 RN [1]

RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=75131227; PubMed=1120493;  
RA Anastasi A., Erspamer V., Endean R.;  
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
RL Experientia 31:394-395(1975).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
|||  
Db 1 QPDP 4

#### RESULT 20

##### TIN2\_HOPTI

ID TIN2\_HOPTI STANDARD; PRT; 12 AA.  
AC P82652;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tigerinin-2.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,

CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT DISULFID 3 11  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 42.9%; Score 18; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7  
 |||  
 Db 7 PLP 9

# RESULT 21

## TIN3\_HOPTI

ID TIN3\_HOPTI STANDARD; PRT; 12 AA.  
 AC P82653;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tigerinin-3.  
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
 OC Hoplobatrachus.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT DISULFID 3 11  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 42.9%; Score 18; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7  
 |||  
 Db 7 PLP 9

# RESULT 22

## PEDI\_HYDAT

ID PEDI\_HYDAT STANDARD; PRT; 13 AA.  
 AC P80578;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Pedin.  
 OS Hydra attenuata (Hydra) (Hydra vulgaris).  
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 OC Hydridae; Hydra.  
 OX NCBI\_TaxID=6087;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96232307; PubMed=8674432;  
 RA Hoffmeister S.A.H.;  
 RT "Isolation and characterization of two new morphogenetically active  
 RT peptides from Hydra vulgaris.";  
 RL Development 122:1941-1948(1996).  
 CC -!- FUNCTION: Morphogenetically active peptide. Active in foot  
 CC development.  
 KW Morphogen.  
 SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 42.9%; Score 18; DB 1; Length 13;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQPPPLP 7  
 : : | |  
 Db 3 LRPEVLP 9

# RESULT 23

## ECDC\_LYMDI

ID ECDC\_LYMDI STANDARD; PRT; 14 AA.  
 AC P80940;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Testis ecdysiotropin peptide C (TE).  
 OS Lymantria dispar (Gypsy moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
 OC Lymantriidae; Lymantria.  
 OX NCBI\_TaxID=13123;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=97387807; PubMed=9243792;  
 RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
 RA Bell R.A.;  
 RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
 RT gonadotropin isolated from brains of Lymantria dispar pupae.";  
 RL Arch. Insect Biochem. Physiol. 36:37-50(1997).



CC    -!- FUNCTION: Stimulates synthesis of ecdysteroid in the testes of  
CC       larvae and pupae.

SQ   SEQUENCE   14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match                   42.9%; Score 18; DB 1; Length 14;  
Best Local Similarity   100.0%; Pred. No. 1.5e+03;  
Matches       3; Conservative   0; Mismatches    0; Indels       0; Gaps       0;

Qy           5 PLP 7  
              | | |  
Db           9 PLP 11

#### RESULT 24

AF1L\_MALPA

ID   AF1L\_MALPA       STANDARD;       PRT;   15 AA.

AC   P83141;

DT   28-FEB-2003 (Rel. 41, Created)

DT   28-FEB-2003 (Rel. 41, Last sequence update)

DT   28-FEB-2003 (Rel. 41, Last annotation update)

DE   Antifungal protein 1 large subunit (CW-1) (Fragment).

OS   Malva parviflora (Little mallow) (Cheeseweed).

OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC   eurosids II; Malvales; Malvaceae; Malvoideae; Malva.

OX   NCBI\_TaxID=145753;

RN   [1]

RP   SEQUENCE, AND FUNCTION.

RC   TISSUE=Seed;

RX   MEDLINE=20568734; PubMed=11118343;

RA   Wang X., Bunkers G.J.;

RT   "Potent heterologous antifungal proteins from cheeseweed (Malva  
RT   parviflora).";

RL   Biochem. Biophys. Res. Commun. 279:669-673(2000).

CC   -!- FUNCTION: Possesses antifungal activity against P.infestans but  
CC       not F.graminearum.

CC   -!- SUBUNIT: Heterodimer of a large and a small subunit.

CC   -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
CC       concentration.

DR   GO; GO:0003799; F:antifungal peptide activity; IDA.

KW   Fungicide; Antibiotic.

FT   NON\_TER       15       15

SQ   SEQUENCE   15 AA; 1783 MW; 2CB3079F53CC70F9 CRC64;

Query Match                   42.9%; Score 18; DB 1; Length 15;  
Best Local Similarity   100.0%; Pred. No. 1.6e+03;  
Matches       3; Conservative   0; Mismatches    0; Indels       0; Gaps       0;

Qy           4 PPL 6  
              | | |  
Db           8 PPL 10

#### RESULT 25

MK1\_PALPR

ID   MK1\_PALPR       STANDARD;       PRT;   15 AA.

AC   P80408;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metalnikowin I.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -!- INDUCTION: By bacterial infection.  
 KW Antibiotic; Insect immunity.  
 SQ SEQUENCE 15 AA; 1838 MW; 21407E663CE46299 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
 :| | |  
 Db 7 RPRPRP 12

#### RESULT 26

##### MK2A\_PALPR

ID MK2A\_PALPR STANDARD; PRT; 15 AA.  
 AC P80409;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Metalnikowin IIA.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
 OC Palomena.  
 OX NCBI\_TaxID=55431;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.

CC -!- INDUCTION: By bacterial infection.  
KW Antibiotic; Insect immunity.  
SQ SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:| | |  
Db 7 RPRPWP 12

#### RESULT 27

##### FOR1\_MYRGU

ID FOR1\_MYRGU STANDARD; PRT; 16 AA.  
AC P81438;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Formaecin 1.  
OS Myrmecia gulosa (Red bulldog ant).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Formicidae; Myrmeciinae; Myrmeciini; Myrmecia.  
OX NCBI\_TaxID=36170;  
RN [1]  
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
RC TISSUE=Hemolymph;  
RX MEDLINE=98165787; PubMed=9497332;  
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
RT "Isolation from an ant Myrmecia gulosa of two inducible  
RT O-glycosylated proline-rich antibacterial peptides."  
RL J. Biol. Chem. 273:6139-6143(1998).  
CC -!- FUNCTION: Antibacterial peptide. Has activity against E.coli  
CC but none against other Gram-negative bacteria and Gram-positive  
CC bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By bacterial infection.  
CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.  
KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;

Query Match 42.9%; Score 18; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:| | |  
Db 9 KPTPHP 14

#### RESULT 28

##### MK2B\_PALPR

ID MK2B\_PALPR STANDARD; PRT; 16 AA.  
AC P80410;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Metalnikowin IIB.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
OC Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin.";  
RL J. Insect Physiol. 42:81-89(1996).  
CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
CC -!- INDUCTION: By bacterial infection.  
KW Antibiotic; Insect immunity.  
SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QPPPLP 7  
:| | |  
Db 7 RPRPWP 12

# RESULT 29

MK3\_PALPR  
ID MK3\_PALPR STANDARD; PRT; 16 AA.  
AC P80411;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Metalnikowin III.  
OS Palomena prasina (Green shield bug).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;  
OC Palomena.  
OX NCBI\_TaxID=55431;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Hemolymph;  
RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
RT "The inducible antibacterial peptides of the hemipteran insect  
RT Palomena prasina: identification of a unique family of proline-rich  
RT peptides and of a novel insect defensin.";  
RL J. Insect Physiol. 42:81-89(1996).

CC -!- FUNCTION: Antibacterial peptide active against Gram-negative  
CC bacteria.  
CC -!- INDUCTION: By bacterial infection.  
KW Antibiotic; Insect immunity.  
SQ SEQUENCE 16 AA; 2024 MW; A9E3835D063B9462 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
:| | |  
Db 7 RPRPWP 12

#### RESULT 30

##### BPP8\_BOTIN

ID BPP8\_BOTIN STANDARD; PRT; 10 AA.  
AC P30426;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom."  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; H37196; H37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QPPPLP 7  
| | :|  
Db 4 QHPNIP 9

#### RESULT 31

##### LADD\_ONCMY

ID LADD\_ONCMY STANDARD; PRT; 11 AA.  
AC P81018;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Ladderlectin (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=97293418; PubMed=9149391;  
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;  
RT "A rainbow trout lectin with multimeric structure.";  
RL Comp. Biochem. Physiol. 116B:385-390(1997).  
CC -!- FUNCTION: Lectin that binds sepharose.  
CC -!- COFACTOR: Calcium is essential for sepharose binding.  
CC -!- SUBUNIT: Multimeric.  
KW Lectin; Calcium.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
| |  
Db 7 QXPP 10

#### RESULT 32

##### TKN1\_PSEGU

ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-I (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC !- SUBCELLULAR LOCATION: Secreted.  
 CC !- TISSUE SPECIFICITY: Skin.  
 CC !- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; B60409; B60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
 |||  
 Db 1 QPHP 4

### RESULT 33

#### TKN2\_PSEGU

ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42987;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC !- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC !- SUBCELLULAR LOCATION: Secreted.  
 CC !- TISSUE SPECIFICITY: Skin.  
 CC !- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; C60409; C60409.

DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
 |||  
 Db 1 QPNP 4

#### RESULT 34

##### TKN3\_PSEGU

ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.



FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
 |||  
 Db 1 QPHP 4

# RESULT 35

## TKN4\_PSEGU

ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide I (PG-SPI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; E60409; E60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
|||  
Db 1 QPNP 4

RESULT 36

TKN5\_PSEGU

ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
AC P42990;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P-like peptide II (PG-SPII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guntheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; F60409; F60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
|||  
Db 1 QPNP 4

RESULT 37

## TKN2\_KASMA

ID TKN2\_KASMA STANDARD; PRT; 12 AA.  
 AC P08614;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hylambatin.  
 OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;  
 OC Kassina.  
 OX NCBI\_TaxID=8414;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;  
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and  
 RT hylambatin, in the skin of the African rhacophorid frog Hylambates  
 RT maculatus.";  
 RL Biomed. Res. 2:613-617(1981).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S07436; S07436.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
 |||  
 Db 2 PPDP 5

## RESULT 38

## GER1\_HORVU

ID GER1\_HORVU STANDARD; PRT; 13 AA.  
 AC P28525;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS1 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;

RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress.";  
 RL Plant Physiol. 97:366-374(1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell  
 CC walls during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in  
 CC the mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPL 6  
 | ||  
 Db 3 PSPL 6

#### RESULT 39

##### GER2\_HORVU

ID GER2\_HORVU STANDARD; PRT; 13 AA.  
 AC P28526;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Germin GS2 (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. CM 72; TISSUE=Root;  
 RA Hurkman W.J., Tao H.P., Tanaka C.K.;  
 RT "Germin-like polypeptides increase in barley roots during salt  
 RT stress.";  
 RL Plant Physiol. 97:366-374(1991).  
 CC -!- FUNCTION: May play a role in altering the properties of cell walls  
 CC during germinative growth.  
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)

CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.  
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the  
 CC mature region, but not in the tip. Not detected in leaves.  
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt  
 CC stress in coleoptile.  
 CC -!- PTM: Glycosylated.  
 CC -!- SIMILARITY: Belongs to the germin family.  
 DR InterPro; IPR001929; Germin.  
 DR PROSITE; PS00725; GERMIN; PARTIAL.  
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.  
 FT UNSURE 10 10  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PPPL 6  
 | ||  
 Db 3 PSPL 6

#### RESULT 40

##### SODM\_CANFA

ID SODM\_CANFA STANDARD; PRT; 13 AA.  
 AC P54712;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).  
 GN SOD2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: Destroys radicals which are normally produced within the  
 CC cells and which are toxic to biological systems.  
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).  
 CC -!- SUBUNIT: Homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
 CC family.  
 DR HSC-2DPAGE; P54712; DOG.  
 DR InterPro; IPR001189; SODismutase.  
 DR Pfam; PF00081; sodfe; 1.  
 DR PROSITE; PS00088; SOD\_MN; PARTIAL.

KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1476 MW; 9C9651DE8BE0672A CRC64;

Query Match 40.5%; Score 17; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
| ||  
Db 5 PDLP 8

RESULT 41

SODM\_ENTAE

ID SODM\_ENTAE STANDARD; PRT; 15 AA.  
AC P22799;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).  
GN SODA.  
OS Enterobacter aerogenes (Aerobacter aerogenes).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=548;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91248479; PubMed=1368658;  
RA Kim S.W., Lee S.O., Lee T.H.;  
RT "Purification and characterization of superoxide dismutase from  
RT Aerobacter aerogenes.";  
RL Agric. Biol. Chem. 55:101-108(1991).  
CC -!- FUNCTION: Destroys radicals which are normally produced within the  
CC cells and which are toxic to biological systems.  
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).  
CC -!- SUBUNIT: Homodimer.  
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
CC family.  
DR PIR; P0615; P0615.  
DR InterPro; IPR001189; SODismutase.  
DR Pfam; PF00081; sodfe; 1.  
DR PROSITE; PS00088; SOD\_MN; PARTIAL.  
KW Oxidoreductase; Metal-binding; Iron.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;

Query Match 40.5%; Score 17; DB 1; Length 15;  
Best Local Similarity 75.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
| ||  
Db 5 PQLP 8

# RESULT 42

PPK2\_PERAM

ID PPK2\_PERAM STANDARD; PRT; 8 AA.  
 AC P82692;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=97353923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of two pyrokinins from the  
 RT retrocerebral complex of the American cockroach.";  
 RL Peptides 18:473-478(1997).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.  
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPPLP 7  
 || |  
 Db 2 PPFAP 6

# RESULT 43

FAR9\_ASCSU

ID FAR9\_ASCSU STANDARD; PRT; 9 AA.  
 AC P43172;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF9.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;  
 RA Cowden C., Stretton A.O.W.;  
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
 RT Ascaris suum.";  
 RL Peptides 16:491-500(1995).  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPPL 6  
 | |  
 Db 4 PRPL 7

#### RESULT 44

##### MGMT\_BOVIN

ID MGMT\_BOVIN STANDARD; PRT; 9 AA.  
 AC P29177;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-  
 DE methylguanine-DNA methyltransferase) (Fragment).  
 GN MGMT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karran P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA  
 RT methyltransferase.";  
 RL Nucleic Acids Res. 18:17-21(1990).  
 CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically  
 CC transferring the alkyl group at the O-6 position to a cysteine  
 CC residue in the enzyme. This is a suicide reaction: the enzyme is  
 CC irreversibly inactivated.  
 CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +  
 CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein  
 CC S-methyl-L-cysteine.  
 CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE  
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.



DR InterPro; IPR001497; Methyltransf\_1.  
 DR PROSITE; PS00374; MGMT; PARTIAL.  
 KW DNA repair; Transferase; Methyltransferase.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7  
 |:|  
 Db 2 PIP 4

#### RESULT 45

##### AH3\_PRUSE

ID AH3\_PRUSE STANDARD; PRT; 10 AA.  
 AC P29261;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase  
 DE isozyme II) (AH II) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: Absent from maturing black cherry fruits  
 CC until 6 weeks after flowering. Then, concomitant with cotyledon  
 CC development, the level of enzyme increases with specificity for  
 CC embryonal tissues.  
 CC -!- PTM: Glycosylated.  
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPL 6  
 ||:  
 Db 3 PPI 5

RESULT 46

BPP2\_BOTIN

ID BPP2\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QPPP 5  
 | |  
 Db 7 QIPP 10

RESULT 47

BPP2\_BOTJA

ID BPP2\_BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
 DE inhibitor V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
 RA Kocy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
 RT jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039(1971).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAVI6B.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QPPP 5  
 | ||  
 Db 7 QIPP 10

#### RESULT 48

##### UPA2\_HUMAN

ID UPA2\_HUMAN STANDARD; PRT; 10 AA.  
 AC P30088;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.4, its MW is: 49 kDa.  
 DR SWISS-2DPAGE; P30088; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 6 6  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQPP 4  
: ||  
Db 3 LSPP 6

RESULT 49

TIN1\_HOPTI

ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerinin-1.  
OS *Hoplobatrachus tigerinus* (Indian bull frog) (*Rana tigerina*).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC *Hoplobatrachus*.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*  
RT *tigerina*.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,  
CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.  
FT DISULFID 2 10  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 11;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PLP 7  
|:|  
Db 6 PIP 8

RESULT 50

TM2A\_METMA

ID TM2A\_METMA STANDARD; PRT; 12 AA.  
AC P80652;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M  
DE methyltransferase 28 kDa subunit) (Fragment).

OS Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;  
 OC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
 RT coenzyme M methyltransferase from Methanosarcina mazei Go1  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).  
 CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.  
 CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
 CC (methylthio)ethanesulfonate.  
 CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 38.1%; Score 16; DB 1; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPLP 7  
 | | |  
 Db 6 PVLP 9

Search completed: July 4, 2004, 04:41:24  
 Job time : 5.40299 secs